

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 11, 2001, 14:01:44 ; Search time 20.34 Seconds
(without alignments)
132.536 Million cell updates/sec

Title: US-09-164-223-2

Perfect score: 123

Sequence: 1 PSQASSGQARMPNAPYLPSGLE 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SPREMBL.15:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp.invertebrate:*
7: sp.mammal:*
8: sp.mhnc:*
9: sp.organelle:*
10: sp.phage:*
11: sp.plant:*
12: sp.rodent:*
13: sp.virus:*
14: sp.vertebrate:*
15: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	123	100.0	446	4	Q15881
2	103	83.7	407	3	P79958
3	102	82.9	390	13	O42223
4	99	80.5	392	13	O91030
5	99	80.5	414	13	O918A1
6	99	80.5	417	13	O918A0
7	95	77.2	409	13	O91657
8	85	69.1	426	13	O9W611
9	82	66.7	392	13	O9IB80
10	65	52.8	392	13	O93433
11	63	51.2	419	13	O9P077
12	48	39.0	188	4	O14901
13	48	39.0	188	4	O14901
14	48	39.0	778	12	O84509
15	47.5	38.6	65	6	O46611
16	47.5	38.6	250	6	O95417
17	47	38.2	115	5	O16031
18	47	38.2	405	10	O41516
19	47	38.2	405	10	O9SYX0

20	47	38.2	815	10	Q41553
21	47	38.2	830	10	Q03872
22	47	38.2	3381	2	O9KX33
23	46	37.4	374	5	O26665
24	46	37.4	606	8	O9TA19
25	46	37.4	766	10	O9SDM3
26	46	37.4	955	11	O88287
27	45.5	37.0	704	5	O45750
28	45	36.6	320	2	O56299
29	45	36.6	381	10	O41556
30	45	36.6	385	2	O54913
31	45	36.6	388	14	O35997
32	45	36.6	401	14	O35996
33	45	36.6	488	5	O9TYR3
34	45	36.6	572	11	O61090
35	45	36.6	2075	5	O9VXY2
36	44	35.8	225	12	P87542
37	44	35.8	292	2	O25957
38	44	35.8	292	2	O92UK7
39	44	35.8	343	5	O18636
40	44	35.8	393	5	O18880
41	44	35.8	395	5	O26913
42	44	35.8	449	5	O00819
43	44	35.8	455	2	O31345
44	44	35.8	459	5	O905V4
45	44	35.8	472	10	O9SN50

ALIGNMENTS

RESULT	ID	PRELIMINARY:	PRT:	446 AA.
Q15881	Q15881			
AC	Q15881			
DT	01-NOV-1996 (TRENBLREL. 01, Created)			
DT	01-NOV-1996 (TRENBLREL. 01, Last sequence update)			
DT	01-OCT-2000 (TRENBLREL. 15, Last annotation update)			
DE	WILMS TUMOR PROTEIN.			
GN	WT1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92241883; PubMed=1572653;			
RA	Gessler M., Konig A., Bruns G.A.;			
RT	"The genomic organization and expression of the WT1 gene.";			
RL	Genomics 12:807-813(1992).			
DR	EMBL; X61631; CAA43819.1; JOINED.			
DR	EMBL; X61632; CAA43819.1; JOINED.			
DR	EMBL; X61633; CAA43819.1; JOINED.			
DR	EMBL; X61634; CAA43819.1; JOINED.			
DR	EMBL; X61635; CAA43819.1; JOINED.			
DR	EMBL; X61636; CAA43819.1; JOINED.			
DR	EMBL; X61637; CAA43819.1; JOINED.			
DR	EMBL; X61638; CAA43819.1; JOINED.			
DR	HSSP: P08046; 1AAY.			
DR	INTERPRO: IPR000822; -			
DR	INTERPRO: IPR000976; -			
DR	PFAM: PF00096; z1-C2H2; 4.			
DR	PFAM: PF02165; WT1; 1.			
DR	PRINTS: PR00048; ZINCINGER.			
DR	PRINTS: PR00049; WILMSTUMOUR.			
DR	PROSITE: PS00028; ZINC_FINGER_C2H2; 4.			
DR	ZINC_Finger; Metal-binding; DNA-binding.			
KW	SEQUENCE 446 AA; 48842 MW; 8CE7FC047FA1CF11 CRC64;			
SO				

Query Match 100.0%; Score 123; DB 4; Length 446;
Best Local Similarity 100.0%; Pred. No. 2e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PSQASSGQARMPNAPYLPSCLE 23
 DB 117 PSQASSGQARMPNAPYLPSCLE 139

RESULT 2

P79958 PRELIMINARY; PRT; 407 AA.

AC P79958:
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE WT1 PROTEIN.

GN

OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8355;

RP SEQUENCE FROM N.A.

RC TISSUE-TESTIS.

RX MEDLINE=97074667; PubMed=9917094;
 RA Senda K., Saito-Ueno R., Takayama G., Kondo M.;
 RT "cDNA cloning and its prionephorus-specific expression of the Wilms'
 tumor suppressor gene, WT1, from Xenopus laevis.";
 RL Gene 175:167-172(1996).

DR EMBL: D82051; BAA11522.1; -.

DR HSSP: P08046; 1AAY.

DR INTERPRO: IPR000822; -.

DR INTERPRO: IPR000976; -.

DR PFAM: PF00096; zf-C2H2; 4.

DR PFAM: PF02165; WT1; 3.

DR PRINTS: PR00048; ZINC_FINGER.

DR PROSITE: PS00028; ZINC_FINGER_C2H2; 4.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

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DR zinc-finger; Metal-binding; DNA-binding.

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DR zinc-finger; Metal-binding; DNA-binding.

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DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR PROSITE: PS00028; ZINC_FINGER_C2H2; 3.
 KW zinc-finger; Metal-binding; DNA-binding.
 SQ SEQUENCE 390 AA; 43620 MW; 1C9987435BE927C2 CRC64;

Query Match 82.9%; Score 103; DB 13; Length 390;
 Best Local Similarity 78.3%; Pred. No. 3; 4e-08;
 Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 PSQASSGQARMPNAPYLPSCLE 23
 DB 100 PTOAPSSGQARMPNAPYLPSCLE 122

RESULT 4

O91030 PRELIMINARY; PRT; 392 AA.

AC O91030:
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE CHICK WILM'S TUMOUR PROTEIN (FRAGMENT).
 DE WT1 (-KTS).

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RP SEQUENCE FROM N.A.

RC TISSUE-WHOLE EMBRYO;

RX MEDLINE=96068905; PubMed=7478606;

RA Kent J., Coriat A.M., Sharpe P.T., Hastie N., Van Heyningen V.;

RT "The evolution of WT1 sequence and expression pattern in the

vertebrates.";

RL Oncogene 11:1781-1792(1995).

DR EMBL: X85731; CAA59736.1; -.

DR HSSP: P08046; 1AAY.

DR INTERPRO: IPR000822; -.

DR INTERPRO: IPR000976; -.

DR PFAM: PF00096; zf-C2H2; 3.

DR PFAM: PF02165; WT1; 2.

DR PRINTS: PR00049; WILMSTUMOUR.

DR PROSITE: PS00028; ZINC_FINGER_C2H2; 3.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

Query Match 83.7%; Score 103; DB 13; Length 407;
 Best Local Similarity 78.3%; Pred. No. 2; 5e-08;
 Matches 18; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 PSQASSGQARMPNAPYLPSCLE 23
 DB 98 PSQATTCQARMPNAPYLPSCLE 120

RESULT 3

O42223 PRELIMINARY; PRT; 390 AA.

AC O42223:
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE WILMS TUMOR 1 PROTEIN.

GN

OS Trachemys scripta (Red-eared slider turtle).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Testudines; Cryptodira; Testudinoidae; Emydidae; Trachemys.

OX NCBI_TaxID=34903;

RP SEQUENCE FROM N.A.

RA Spottila L.D., Hall S.E.;

RT Submitted (Aug-1997) to the EMBL/Genbank/DBJ databases.

DE EMBL: AF019779; AAB70832.1; -.

DR HSSP: P08046; 1AAY.

DR INTERPRO: IPR000822; -.

DR INTERPRO: IPR000976; -.

DR PFAM: PF00096; zf-C2H2; 4.

DR PFAM: PF02165; WT1; 2.

DR PRINTS: PR00048; ZINC_FINGER.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

DR zinc-finger; Metal-binding; DNA-binding.

Query Match 80.5%; Score 99; DB 13; Length 392;
 Best Local Similarity 78.3%; Pred. No. 1e-07;
 Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 PSQASSGQARMPNAPYLPSCLE 23
 DB 100 PSQPPSGQARMPNAPYLPSCLE 122

RESULT 5

O918A1 PRELIMINARY; PRT; 414 AA.

AC O918A1:
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE WT1 (-KTS).

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RP SEQUENCE FROM N.A.

RC TISSUE-WHOLE EMBRYO;

RX MEDLINE=96068905; PubMed=7478606;

RA Kent J., Coriat A.M., Sharpe P.T., Hastie N., Van Heyningen V.;

RT "The evolution of WT1 sequence and expression pattern in the

RP SEQUENCE FROM N.A.
 RC TISSUE-Ovary;
 RA Kudo T.;
 RT "Chicken counterpart of Wilms' tumor suppressor gene 1."
 RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AB033633; BAA94793.1;
 SO SEQUENCE 414 AA; 46641 MW; 17BB2F8B428A2EF CRC64;

Query Match 80.5%; Score 99; DB 13; Length 414;
 Best Local Similarity 78.3%; Pred. No. 1.1e-07;
 Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 PSQASSGQARMPNAPYLPSCLE 23
 ||| ||||| ||||| |||
 DB 100 PSQPPSGQARMPORPYLPNCLE 122

RESULT 6

OY18A0 PRELIMINARY; PRT; 417 AA.

AC O918A0:
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE WT1(+KTS) PROTEIN.
 GN WT1(+KTS).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Ovary;
 RA Kudo T.;
 RT "Chicken counterpart of Wilms' tumor suppressor gene 1."
 RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AB033634; BAA94794.1;
 SO SEQUENCE 417 AA; 46957 MW; 47BBF7F6448E76C CRC64;

Query Match 80.5%; Score 99; DB 13; Length 417;
 Best Local Similarity 78.3%; Pred. No. 1.1e-07;
 Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 PSQASSGQARMPNAPYLPSCLE 23
 ||| ||||| ||||| |||
 DB 100 PSQPPSGQARMPORPYLPNCLE 122

RESULT 7

OY1657 PRELIMINARY; PRT; 409 AA.

AC O91657:
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE WILMS' TUMOR SUPPRESSOR (WT1).
 GN WT1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Carroll T.J., Vize P.D.;
 RL Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 289-370 FROM N.A.
 RC TISSUE=MESONEPHROS; PUBMED=7478606;
 MEDLINE=96068905;

RA Kent J., Coriat A.M., Sharpe P.T., Hastie N., Van Heyningen V.;
 RT "The evolution of WT1 sequence and expression pattern in the
 vertebrates."
 RL Oncogene 11:1781-1792(1995).
 DR EMBL: U42011; AAB53152.1;
 DR EMBL: X85733; CAA59738.1;
 DR HSSP: P08046; IAAV.
 DR INTERPRO: IPR000822;
 DR INTERPRO: IPR000976;
 DR PFAM: PF02165; WT1; 3.
 DR PRINTS: PR00048; ZINC_FINGER_C2H2; 4.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2; 4.
 KW Zinc-finger; Metal-binding; DNA-binding.
 SO SEQUENCE 409 AA; 46186 MW; 2217FC04612CDE10 CRC64;

Query Match 77.2%; Score 95; DB 13; Length 409;
 Best Local Similarity 73.9%; Pred. No. 4.5e-07;
 Matches 17; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 PSQASSGQARMPNAPYLPSCLE 23
 ||||| ||||| ||||| |||
 DB 97 PSQATTGQARMPNAPYLPNCLE 119

RESULT 8

OY6611 PRELIMINARY; PRT; 426 AA.

AC OY6611:
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE WT1.
 OS Cynops pyrrhogaster (Japanese common newt).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandridae; Salamandridae; Cynops.
 OX NCBI_TaxID=8330;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-TESTIS;
 RA Nakayama Y., Yamamoto T., Matsuda Y., Abe S.I.;
 RT "Cloning of cDNA for new WT1 and the differential expression during
 spermatogenesis of the Japanese newt, Cynops pyrrhogaster."
 RL Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AB013888; BAA76399.1;
 DR HSSP: P08046; IAAV.
 DR INTERPRO: IPR000822;
 DR INTERPRO: IPR000976;
 DR PFAM: PF00096; ZF-C2H2; 4.
 DR PRINTS: PR00049; WILMSTUMOR.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2; 4.
 KW Zinc-finger; Metal-binding; DNA-binding.
 SO SEQUENCE 426 AA; 47590 MW; 46A0B158A9F79C6C CRC64;

Query Match 69.1%; Score 85; DB 13; Length 426;
 Best Local Similarity 65.2%; Pred. No. 1.7e-07;
 Matches 15; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 PSQASSGQARMPNAPYLPSCLE 23
 ||| : ||| | ||||| |||
 DB 107 PSQPPAQVARMPSNGPYLPNCLE 129

RESULT 9

OY16F0 PRELIMINARY; PRT; 392 AA.

AC O916F0:
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE WILMS' TUMOR PROTEIN.

GN EMT1.
 OS Anguilla japonica (Japanese eel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
 OC Anguilla japonica.
 RN NCB1_TaxID=7937;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY.
 RA Nakatsu Y., Minami K., Yoshikawa A., Zhu J.J., Oda H., Masahito P.,
 RA Okamoto N., Nakamura Y., Ishikawa T.;
 RT "Bel Wt1 sequence and expression in spontaneous nephroblastomas in
 RT Japanese eel."
 RL Gene 245:245-251(2000).
 DR EMBL; AB030741; BAA0558.1;
 SO SEQUENCE 392 AA; 43892 MW; DAELA84828F43DF6 CRC64;

Query Match 66.7%; Score 82; DB 13; Length 392;
 Best Local Similarity 60.9%; Pred. No. 4.8e-05;
 Matches 14; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 1 PSQSSGQARMPNAPYIPSCLE 23
 DB 103 PSQPPGNQARMPANGPILPNCVD 125

RESULT 10
 093433 PRELIMINARY; PRT; 416 AA.
 AC 093433;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE WILMS TUMOUR GENE.
 GN WT1.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Takifugu.
 RN NCB1_TaxID=31033;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Miles C., Elgar G., Coles E., Kleinjan D.J., Vanheyningen V.,
 RA Hastie N.;
 RT "Complete sequencing of the Fugu WAGR region from WT1 to PAX6
 RT -dramatic compaction and conservation of synteny with human chromosome
 RT 11p13."
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL021531; CAAL6491.1;
 DR HSSP; P08046; 1AAY.
 DR INTERPRO; IPR000822;
 DR INTERPRO; IPR000976;
 DR PFAM; PF00096; zF-C2H2; 4.
 DR PFAM; PF02165; WT1; 2.
 DR PRINTS; PR00048; ZINC_FINGER.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2; 4.
 KW Zinc-finger; Metal-binding; DNA-binding.
 SO SEQUENCE 416 AA; 45806 MW; 9C362E1684E67668 CRC64;

Query Match 52.8%; Score 65; DB 13; Length 416;
 Best Local Similarity 61.1%; Pred. No. 0.024;
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 6 SQQARMPNAPYIPSCLE 23
 DB 104 AGQPRMFPNGTCLPSCMD 121

RESULT 11
 09PUT7

ID 09PUT7 PRELIMINARY; PRT; 419 AA.
 AC 09PUT7;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE WILMS TUMOR SUPPRESSOR.
 OS Brachydanio rerio (zebrafish) (zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Rasbora; Danio.
 RN NCB1_TaxID=7955;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Smith S.I., Down M., Power M., Boyd A.W.;
 RT "Isolation and characterization of a cDNA encoding zebrafish (Danio
 RT rerio) WT-1."
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF144550; AAF00123.1;
 DR HSSP; P08046; 1AAY.
 DR INTERPRO; IPR000822;
 DR INTERPRO; IPR000976;
 DR PFAM; PF00096; zF-C2H2; 4.
 DR PFAM; PF02165; WT1; 3.
 DR PRINTS; PR00049; WILMTUMOUR.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2; 4.
 SO SEQUENCE 419 AA; 46925 MW; 606ADFEDA619ECD CRC64;

Query Match 51.2%; Score 63; DB 13; Length 419;
 Best Local Similarity 50.0%; Pred. No. 0.049;
 Matches 11; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 2 SQPPSQPRMFSNPYISNCMD 124
 DB 103 SQPPSQPRMFSNPYISNCMD 124

RESULT 12
 016591 PRELIMINARY; PRT; 188 AA.
 AC 016591;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE C-MYC ONCOGENE, EXON 1.
 GN MYC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN NCB1_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=87048763; PubMed=3778453;
 RA Eladad M.E., Syed S.H., Guilhot S., d'Auriol L., Galibert F.;
 RL "On the high conservation of the human c-myc first exon."
 RL Biochem. Biophys. Res. Commun. 140:313-319(1986).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=84182501; PubMed=6714223;
 RA Gazin C., De Dinechin S., Hampe A., Maesson J.M., Martin P.,
 RA Stehelin D., Galibert F.;
 RT "Nucleotide sequence of the human c-myc locus: provocative open
 RT reading frame within the first exon."
 RL EMBO J. 3:383-387(1984).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC TISSUE=LEUKEMIA;
 RX MEDLINE=88203638; PubMed=2834731;
 RA Finver S.N., Nishikura K., Finger L.R., Halska F.G., Elnan J.,
 RA Nowell P.C., Croce C.M.;
 RT "Sequence analysis of the MYC oncogene involved in the
 RT t(8;14)(q24;q11) chromosome translocation in a human leukemia T-cell
 RT line indicates that putative regulatory regions are not altered.";

RL Proc. Natl. Acad. Sci. U.S.A. 85:3052-3056(1988).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PROMYELOCYTIC LEUKEMIA;
 RX MEDLINE=87089682; PubMed=3540591;
 RA Bentley D.L., Groudine M.;
 RT "Novel promoter upstream of the human c-myc gene and regulation of c-
 MYC expression in B-cell lymphomas."
 RL Mol. Cell. Biol. 6:3481-3489(1986).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84170251; PubMed=6324175;
 RA Saito H., Hayday A.C., Wiman K.G., Tonegawa S.;
 RT "Activation of the c-myc gene by translocation: a model for
 RT translocation control."
 RL Proc. Natl. Acad. Sci. U.S.A. 80:7476-7480(1983).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87053865; PubMed=2430795;
 RA Gazin C., Rigollet M., Briland J.P., Van Regenmortel M.H.V.,
 RA Galibert F.;
 RT "Immunochemical detection of proteins related to the human c-myc exon
 RT 1."
 RL EMBO J. 5:2241-2250(1986).
 DR EMBL; M14206; AAA88090.1; -;
 DR EMBL; J00120; AAA20041.1; -;
 DR EMBL; J03253; AAA59887.1; -;
 DR EMBL; M13930; AAA88094.1; -;
 DR EMBL; X00364; CAA25105.1; -;
 SQ SEQUENCE 188 AA; 20955 MW; 677ADDDAC541477B CRC64;

Query Match 39.0%; Score 48; DB 4; Length 188;
 Best Local Similarity 72.7%; Pred. No. 5;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 PNPAPLPSCLE 23
 Db 22 PGRWPLPSCLE 32

RESULT 13
 Q14901
 ID Q14901 PRELIMINARY; PRT; 188 AA.
 AC 014901;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE MYC PROTEIN.
 GN MYC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LEUKEMIA;
 RX MEDLINE=88203638; PubMed=2834731;
 RA Flinter S.N., Nishikura K., Finger L.R., Haluska F.G., Finan J.,
 RA Nowell P.C., Croce C.M.;
 RT "Sequence analysis of the MYC oncogene involved in the
 RT t(8;14)(q24;q11) chromosome translocation in a human leukemia T-cell
 RT line indicates that putative regulatory regions are not altered."
 RL Proc. Natl. Acad. Sci. U.S.A. 85:3052-3056(1988).
 DR EMBL; M20605; AAA59886.1; -;
 SQ SEQUENCE 188 AA; 21050 MW; 9764637FDF79B00 CRC64;

Query Match 39.0%; Score 48; DB 4; Length 188;
 Best Local Similarity 72.7%; Pred. No. 5;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 PNPAPLPSCLE 23

Db 22 PGRWPLPSCLE 32

RESULT 14
 Q84509
 ID Q84509 PRELIMINARY; PRT; 778 AA.
 AC Q84509;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE PRO-RICH.
 GN A189R.
 OS Paramyxium bursaria chlorella virus 1 (PBCV-1).
 OC Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phycodnavirus.
 OX NCBI_TaxID=10506;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95133167; PubMed=7831789;
 RA Lu Z., Li Y., Zhang Y., Kutish G.F., Rock D.L., Van Etten J.L.;
 RT "Analysis of 45 kb of DNA located at the left end of the chlorella
 RT virus PBCV-1 genome."
 RL Virology 206:339-352(1995).
 DR EMBL; U42580; AAC96557.1; -;
 SQ SEQUENCE 778 AA; 84593 MW; 166C087E14632662 CRC64;

Query Match 39.0%; Score 48; DB 12; Length 778;
 Best Local Similarity 47.1%; Pred. No. 20;
 Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 PSQASSGQARMPNPAPY 17
 Db 170 PKQSASGAGLEKRNPF 186

RESULT 15
 Q46611
 ID Q46611 PRELIMINARY; PRT; 65 AA.
 AC Q46611;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN TYPE 5 (FRAGMENT).
 OS Bubalus bubalus (water buffalo).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bubalus.
 OX NCBI_TaxID=89462;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RIVER TYPE (MURRHA); TISSUE=OVARY;
 RA Beg M.A., Appa Rao K.B.C., Torey S.M.;
 RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF045566; AAC02555.1; -;
 DR INTERPRO; IPR000716; -;
 DR PFAM; PF00086; thyroglobulin_1; 1.
 DR PROSITE; PS00484; THYROGLOBULIN_1; 1.
 FT NON_TER 1 65
 FT NON_TER 1 65
 SQ SEQUENCE 65 AA; 7547 MW; DD2A79A681BF4530 CRC64;

Query Match 38.6%; Score 47.5; DB 6; Length 65;
 Best Local Similarity 55.0%; Pred. No. 2.1;
 Matches 11; Conservative 2; Mismatches 4; Indels 3; Gaps 1;

QY 2 SOASSGQARMPNPAPLPSC 21
 Db 1 AGAS---PRMVPRAPVYLPNC 17

Fri Apr 20 12:06:15 2001

us-09-164-223-2.rspt

Page 6

Search completed: April 11, 2001, 14:03:42
Job time: 118 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 11, 2001, 14:01:59 ; Search time 8.66 Seconds
(without alignments)
85.770 Million cell updates/sec

Title: us-09-164-223-2

Sequence: 1 PSQAASSQAMFNPAPYLPSCLE 23

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	123	100.0	448	WT1_RAT	P49952 ratius norv
2	123	100.0	449	WT1_HUMAN	P19544 homo sapien
3	123	100.0	449	WT1_MOUSE	P22561 mus musculu
4	123	100.0	449	WT1_PIG	O62651 sus scrofa
5	52	42.3	82	9KD_HUMAN	P13994 homo sapien
6	49	39.8	885	YD03_YEAST	O06639 saccharomyc
7	48	39.0	618	IAP2_HUMAN	Q13490 homo sapien
8	47	38.2	271	IBP5_MOUSE	O07079 mus musculu
9	47	38.2	271	IBP5_PIG	Q28985 sus scrofa
10	47	38.2	271	IBP5_RAT	P24594 ratius norv
11	47	38.2	272	IBP5_HUMAN	P24593 homo sapien
12	46	37.4	545	SYK_STRCO	O9X895 streptomyce
13	46	37.4	556	GLI_CHICK	P55678 gallus gall
14	45	36.6	382	KSEL_ECOLI	P42501 escherichia
15	45	36.6	382	KSES_ECOLI	P42214 escherichia
16	45	36.6	537	CPO2_MUSDO	O18635 musca domes
17	44	35.8	602	NU5M_MUSDO	P41309 didelphis m
18	44	35.8	726	NEI1_YEAST	Q12216 saccharomyc
19	44	35.8	738	TREH_HUMAN	P08582 homo sapien
20	44	35.8	188	CR12_HUMAN	P13385 homo sapien
21	43.5	35.4	188	CR12_HUMAN	P51664 homo sapien
22	43.5	35.4	337	G3P_METFE	P10618 methanococ
23	43.5	35.4	91	DEFX_MOUSE	O64263 mus musculu
24	43	35.0	118	YTON_ENTAE	P46381 enterobacte
25	43	35.0	353	TPO_HUMAN	P40225 homo sapien
26	43	35.0	526	BGPI_HUMAN	P13688 homo sapien
27	43	35.0	594	NU5M_HIPAM	O92971 hippopotamu
28	43	35.0	601	NU5M_DASNO	O21353 dasypus nov
29	43	35.0	602	NU5M_MACRO	P92669 macropus ro
30	43	35.0	603	NU5M_RABIT	O79437 oncotolagus
31	43	35.0	604	NU5M_HORSE	P48656 equus cabal
32	43	35.0	606	NU5M_BALMU	P41299 balaeopter
33	43	35.0	606	NU5M_BALPH	P24978 balaeopter

34	43	35.0	606	1	NU5M_BOVIN	P03920 bos taurus
35	43	35.0	606	1	NU5M_CANFA	O92557 canis fam11
36	43	35.0	606	1	NU5M_CERSI	O03205 ceratotheri
37	43	35.0	606	1	NU5M_EQUAS	P92485 equus asinu
38	43	35.0	606	1	NU5M_FELCA	P48921 felis silve
39	43	35.0	606	1	NU5M_RHION	O96069 rhinoceros
40	43	35.0	606	1	NU5M_SHEEP	O78766 ovis aries
41	43	35.0	607	1	NU5M_CARAU	O78688 carassius a
42	43	35.0	607	1	NU5M_MOUSE	P03921 mus musculu
43	43	35.0	609	1	NU5M_HALCR	P38602 halichoerus
44	43	35.0	609	1	NU5M_PHOVI	O00542 phoca vitul
45	43	35.0	609	1	NU5M_SCYCA	O79411 scyllorhinu

ALIGNMENTS

RESULT	1	WT1_RAT	STANDARD	PRT	448 AA
WT1_RAT	WT1_RAT				
AC	P49952;				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DT	01-OCT-2000 (Rel. 40, Last annotation update)				
DE	WILMS' TUMOR PROTEIN HOMOLOG.				
GN	WT1 OR WT-1.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=SPRAUE-DAWLEY; TISSUE=KIDNEY;				
RA	MEDLINE=93046155; PubMed=1350293;				
FX	Sharma P.M., Yang X., Bowman M., Roberts V., Sukumar S.;				
RT	"Molecular cloning of rat Wilms' tumor complementary DNA and a study				
RT	of messenger RNA expression in the urogenital system and the brain.";				
RL	Cancer Res. 52:6407-6412(1992)				
CC	-1- FUNCTION: POTENTIAL ROLE IN TRANSCRIPTIONAL REGULATION. RECOGNIZES				
CC	AND BINDS TO THE DNA SEQUENCE 5'-GGCCCCGC-3'.				
CC	-1- SUBCELLULAR LOCATION: NUCLEAR.				
CC	-1- ALTERNATIVE PRODUCTS: TWO ALTERNATIVE SPLICING SITES EXISTS.				
CC	-1- TISSUE SPECIFICITY: KIDNEY (BY SIMILARITY).				
CC	-1- DEVELOPMENTAL STAGE: EXPRESSED DURING KIDNEY DEVELOPMENT.				
CC	-1- SIMILARITY: BELONGS TO THE EGR FAMILY OF C2H2-TYPE ZINC-FINGER				
CC	PROTEINS.				
CC	-----				
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CC	-----				
CC	EMBL: X69716; CAA49373.1; -				
DR	TRANSFAC: T02352; -				
DR	INTERPRO: IPR000822; -				
DR	INTERPRO: IPR000976; -				
DR	PFAM: PF00096; ZF-C2H2; 4.				
DR	PRINTS: PR00048; ZINC-FINGER.				
DR	PRINTS: PR00049; WILMSTUMOR.				
DR	PROSITE: PS00028; ZINC-FINGER C2H2; 4.				
KW	Zinc-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein;				
KW	Transcription regulation; Alternative splicing; Anti-oncogene.				
FT	DOMAIN 27				
FT	DOMAIN 82				
FT	DOMAIN 322				
FT	ZN_FING 322				
FT	ZN_FING 346				
FT	ZN_FING 352				
FT	ZN_FING 382				
FT	ZN_FING 404				
FT	ZN_FING 413				
FT	VARSPIC 437				
FT	VARSPIC 249				
FT	VARSPIC 407				
FT	SEQUENCE 448 AA; 49193 MW; 329AC9AC1F73E76 CRC64;				

Query Match 100.0%; Score 123; DB 1; Length 448;
 Best Local Similarity 100.0%; Pred. No. 1,4e-11;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 1 PSQASSGQARMFPNAPYLPSCLE 23
 ||||||||||||||||||
 Db 116 PSQASSGQARMFPNAPYLPSCLE 138

RESULT 2
 WTL_HUMAN STANDARD: PRT: 449 AA.

AC P19544;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE WILMS' TUMOR PROTEIN (WT33).
 GN WTL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-FETAL KIDNEY;
 RX MEDLINE=90158822; PubMed=2154702;
 RA Gessler M., Poustka A., Cavenee W., Neve R.L., Orkin S.H.,
 RT Bruns G.A.P.;
 RT "Homozygous deletion in Wilms tumours of a zinc-finger gene
 RT identified by chromosome jumping.";
 RL Nature 343:774-778(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RX MEDLINE=92052142; PubMed=1658787;
 RA Haber D.A., Sohn R.L., Buckler A.J., Pelletier J., Call K.M.,
 RT Housman D.E.;
 RT "Alternative splicing and genomic structure of the Wilms tumor gene
 RT WTL.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:9618-9622(1991).
 RN [3]
 RP SEQUENCE OF 85-449 FROM N.A.
 RX MEDLINE=90150277; PubMed=2154355;
 RA Call K.M., Glaser T., Ito C.Y., Buckler A.J., Pelletier J.,
 RT Haber D.A., Rose E.A., Kral A., Yeager H., Lewis W.H., Jones C.,
 RT Housman D.E.;
 RT "Isolation and characterization of a zinc finger polypeptide gene at
 RT the human chromosome 11 Wilms' tumor locus.";
 RL Cell 60:509-520(1990).
 RN [4]
 RP IDENTIFICATION OF START CODON AND ALTERNATIVE SPLICE SITES.
 RX MEDLINE=91141522; PubMed=1671709;
 RA Buckler A.J., Pelletier J., Haber D.A., Glaser T., Housman D.E.,
 RT "Isolation, characterization, and expression of the murine Wilms'
 RT tumor gene (WTL) during kidney development.";
 RL Mol. Cell. Biol. 11:1707-1712(1991).
 RN [5]
 RP VARIANT WT CYS-366.
 RX MEDLINE=92279213; PubMed=1317572;
 RA Little M.H., Prosser J., Condie A., Smith P.J., van Heyningen V.,
 RT "Zinc finger point mutations within the WTL gene in Wilms tumor
 RT patients.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:4791-4795(1992).
 RN [6]
 RP VARIANTS DDS.
 RX MEDLINE=92005721; PubMed=1655284;
 RA Pelletier J., Breuning W., Kashtan C.E., Mauer S.M., Manivel J.C.,
 RT Striegler J.E., Houghton D.C., Jundt C., Habib R., Fouser L.,
 RT Fine R.N., Silverman B.L., Haber D.A., Housman D.;
 RT "Germline mutations in the Wilms' tumor suppressor gene are
 RT associated with abnormal urogenital development in Denys-Drash

RT syndrome.";
 RL Cell 67:437-447(1991).
 RN [7]
 RP VARIANTS DDS.
 RX MEDLINE=93265053; PubMed=1338906;
 RA Baird P.N., Santos A., Groves N., Jadresic L., Cowell J.K.;
 RT "Constitutional mutations in the WTL gene in patients with
 RT Denys-Drash syndrome.";
 RL Hum. Mol. Genet. 1:301-305(1992).
 RN [8]
 RP VARIANTS DDS.
 RX MEDLINE=93271983; PubMed=8388765;
 RA Little M.H., Williamson K.A., Mannens M., Kelsey A., Gosden C.,
 RT Hastie N., van Heyningen V.;
 RT "Evidence that WTL mutations in Denys-Drash syndrome patients may act
 RT in a dominant-negative fashion.";
 RL Hum. Mol. Genet. 2:259-264(1993).
 RN [9]
 RP VARIANT MESOTHELIOMA GLY-273.
 RX MEDLINE=94004972; PubMed=8401592;
 RA Park S., Schalling M., Bernard A., Maheswaran S., Shipley G.C.,
 RA Roberts D., Fletcher J., Shipman R., Rheinwald J., Demetri G.,
 RA Griffin J., Minden M., Housman D.E., Haber D.A.;
 RT "The Wilms tumor gene WTL is expressed in murine mesoderm-derived
 RT tissues and mutated in a human mesothelioma.";
 RL Nat. Genet. 4:415-420(1993).
 RN [10]
 RP VARIANTS WT SER-181 AND ALA-253.
 RX MEDLINE=97268681; PubMed=9108089;
 RA Schmacher V., Schneider S., Fligge A., Wildhardt G., Harms D.,
 RA Schmidt D., Weirich A., Ludwig R., Royer-Pokora B.;
 RT "Correlation of germ-line mutations and two-hit inactivation of the
 RT WTL gene with Wilms tumors of stromal-predominant histology.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:3972-3977(1997).
 RN [11]
 RP VARIANTS DMS TYR-377; LEU-383 AND ASN-396.
 RX MEDLINE=98198341; PubMed=9529364;
 RA Jeanpierre C., Denamur E., Henry I., Cabanis M.-O., Luce S.,
 RA Cecille A., Elion J., Peuchmaur M., Lorat C., Maudet P.,
 RA Gubler M.-C., Jundt C.;
 RT "Identification of constitutional WTL mutations, in patients with
 RT isolated diffuse mesangial sclerosis, and analysis of
 RT genotype/phenotype correlations by use of a computerized mutation
 RT database.";
 RL Am. J. Hum. Genet. 62:824-833(1998).
 RN [12]
 RP REVIEW.
 RX MEDLINE=92207913; PubMed=1313285;
 RA Haber D.A., Buckler A.J.;
 RT "WTL: a novel tumor suppressor gene inactivated in Wilms' tumor.";
 RL New Biol. 4:97-106(1992).
 RN [13]
 RP REVIEW.
 RX MEDLINE=93345769; PubMed=8393820;
 RA Rauscher F.J. III;
 RT "The WTL Wilms tumor gene product: a developmentally regulated
 RT transcription factor in the kidney that functions as a tumor
 RT suppressor.";
 RL FASEB J. 7:896-903(1993).
 CC -1- FUNCTION: POTENTIAL ROLE IN TRANSCRIPTIONAL REGULATION. RECOGNIZES
 CC AND BINDS TO THE DNA SEQUENCE 5'-CGCCCCCGC-3'.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- ALTERNATIVE PRODUCTS: TWO ALTERNATIVE SPLICE SITES EXISTS.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE KIDNEY AND A SUBSET OF
 CC HEMATOPOIETIC CELLS.
 CC -1- DISEASE: WILMS TUMOR (WT) IS AN EMBRYONAL MALIGNANCY OF THE
 CC KIDNEY THAT AFFECTS APPROXIMATELY 1 IN 10,000 INFANTS AND YOUNG
 CC CHILDREN. IT OCCURS BOTH IN SPORADIC AND HEREDITARY FORMS.
 CC INACTIVATION OF WTL IS ONE OF THE CAUSES OF WILMS TUMOR.
 CC -1- DISEASE: PATIENTS WITH DENYS-DRASH SYNDROME (DDS), WHICH IS
 CC CHARACTERIZED BY A TYPICAL NEPHROPATHY AND GENITAL ABNORMALITIES,
 CC HAVE DEFECTS IN THE WTL GENE.
 CC -1- DISEASE: DEFECTS IN WTL ARE ALSO A CAUSE OF DIFFUSE MESANGIAL

CC	SCLEROSIS (DMS), A FORM A DDS.
CC	-1- SIMILARITY: BELONGS TO THE EGR FAMILY OF C2H2-TYPE ZINC-FINGER
CC	PROTEINS.
CC	-1- DATABASE: NAME=WT1; NOTE=WT1 mutation database;
CC	WWW="http://www.umd.necker.fr:2003/"
CC	
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; X51630; CAA35956.1; ALT_INT.
DR	EMBL; M80232; AAA61299.1; JOINED.
DR	EMBL; M80217; AAA61299.1; JOINED.
DR	EMBL; M80218; AAA61299.1; JOINED.
DR	EMBL; M80219; AAA61299.1; JOINED.
DR	EMBL; M80220; AAA61299.1; JOINED.
DR	EMBL; M80221; AAA61299.1; JOINED.
DR	EMBL; M80228; AAA61299.1; JOINED.
DR	EMBL; M80229; AAA61299.1; JOINED.
DR	EMBL; M80231; AAA61299.1; JOINED.
DR	EMBL; M30393; AAA36810.1; JOINED.
DR	PIR; A34673; A34673.
DR	PIR; S08273; S08273.
DR	TRANSFAC; T00899; -.
DR	MIM; I94070; -.
DR	MIM; I94080; -.
DR	MIM; I256370; -.
DR	INTERPRO; IPR000822; -.
DR	INTERPRO; IPR000976; -.
DR	PFAM; PF00096; ZF-C2H2; 4.
DR	PRINTS; PR00048; ZINC-FINGER.
DR	PRINTS; PR00049; WILMSTUMOUR.
DR	PROSITE; PS00028; ZINC_FINGER_C2H2; 4.
KW	Zinc-finger; Metal-binding; Repeat; Nuclear protein;
KW	Transcription regulation; Alternative splicing; Anti-oncogene;
KW	Disease mutation.
FT	DOMAIN 27 83 PRO-RICH.
FT	FT 323 438 ZINC FINGERS.
FT	FT 323 347 C2H2-TYPE.
FT	FT 353 377 C2H2-TYPE.
FT	FT 383 405 C2H2-TYPE.
FT	FT 414 438 C2H2-TYPE.
FT	FT 250 266 MISSING (IN ISOFORM 2 AND ISOFORM 3).
FT	FT 408 410 MISSING (IN ISOFORM 2 AND ISOFORM 4).
FT	FT 181 181 P -> S (IN WT).
FT	FT VARIANT /FTId=VAR_007739.
FT	FT 223 223 S -> N (IN WT).
FT	FT VARIANT /FTId=VAR_007740.
FT	FT 253 253 G -> A (IN WT).
FT	FT VARIANT /FTId=VAR_007741.
FT	FT 273 273 S -> G (IN MESOTHELIOMA).
FT	FT VARIANT /FTId=VAR_007742.
FT	FT 330 330 C -> Y (IN DDS).
FT	FT VARIANT /FTId=VAR_007743.
FT	FT 360 360 C -> G (IN DDS).
FT	FT VARIANT /FTId=VAR_007744.
FT	FT 366 366 R -> C (IN WT).
FT	FT VARIANT /FTId=VAR_007745.
FT	FT 366 366 R -> H (IN DDS).
FT	FT VARIANT /FTId=VAR_007746.
FT	FT 373 373 H -> Q (IN DDS).
FT	FT VARIANT /FTId=VAR_007747.
FT	FT 377 377 H -> Y (IN DDS/DMS).
FT	FT VARIANT
QY	Query Match 100.0%; Score 123; DB 1; Length 449;
	Best Local Similarity 100.0%; Pred. No. 1,4e-11;
	Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	1 PSQASSGQARMPNAPYLPSCLE 23

RESULT	3	
WT1_MOUSE	STANDARD;	PRT: 449 AA.
AC	P22561;	
DT	01-AUG-1991 (Rel. 19, Created)	
DT	01-AUG-1991 (Rel. 19, Last sequence update)	
DT	01-OCT-2000 (Rel. 40, Last annotation update)	
DE	WILMS' TUMOR PROTEIN HOMOLOG.	
OS	WT1 OR Wt-1.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=91141522; PubMed=1671709;	
RT	Buckler A.J., Pelletier J., Haber D.A., Glaser T., Housman D.E.;	
SA	"Isolation, characterization, and expression of the murine Wt1's	
SA	tumor gene (WT1) during kidney development."	
RL	Mol. Cell. Biol. 11:1707-1712(1991).	
CC	-I- FUNCTION: POTENTIAL ROLE IN TRANSCRIPTIONAL REGULATION. RECOGNIZES	
CC	AND BINDS TO THE DNA SEQUENCE 5'-CGCCCCGC-3'.	
CC	-I- SUBCELLULAR LOCATION: NUCLEAR.	
CC	-I- ALTERNATIVE PRODUCTS: TWO ALTERNATIVE SPLICE SITES EXISTS.	
CC	-I- TISSUE SPECIFICITY: KIDNEY.	
CC	-I- DEVELOPMENTAL STAGE: EXPRESSED DURING KIDNEY DEVELOPMENT.	
CC	-I- SIMILARITY: BELONGS TO THE EGR FAMILY OF C2H2-TYPE ZINC-FINGER	
CC	PROTEINS.	
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
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CC	use by non-profit institutions as long as its content is in no way	
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CC	entities requires a license agreement (See http://www.isb-slb.ch/announce/	
CC	or send an email to license@isb-slb.ch).	
CC	-----	
CC	EMBL; M55512; AAA40573.1; -.	
DR	PIR; A39692; A39692.	
DR	TRANSPAC; T02351; -.	
DR	MCD; MGI:98968; WT1.	
DR	INTERPRO; IPR000822; -.	
DR	INTERPRO; IPR000976; -.	
DR	PFAM; PF00006; Zf-C2H2; 4.	
DR	PRINTS; PR00048; ZINC-FINGER.	
DR	PRINTS; PR00049; WILMS-TUMOR.	
DR	PROSITE; PS00028; ZINC-FINGER_C2H2; 4.	
RW	Zinc-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein;	
RW	Transcription regulation; Alternative splicing; Anti-oncogene.	
RW	DOMAIN	28 83
FT	DOMAIN	323 438 ZINC FINGERS.
FT	ZN_FING	323 347 C2H2-TYPE.
FT	ZN_FING	353 377 C2H2-TYPE.
FT	ZN_FING	383 405 C2H2-TYPE.
FT	ZN_FING	414 438 C2H2-TYPE.
FT	VARSPLIC	250 266 MISSING (IN ISOFORM 2 AND ISOFORM 3).
FT	VARSPLIC	408 410 MISSING (IN ISOFORM 2 AND ISOFORM 4).
SO	SEQUENCE	449 AA; 49246 MW; 962381E9C8D7A380 CRC64;
Query Match	100.0%;	Score 123; DB 1; Length 449;
Best Local Similarity	100.0%;	Pred. No. 1,4e-11;
Matches	23; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 PSQASSGOARMPNAPYLPSCLE 23	
DB	117 PSQASSGOARMPNAPYLPSCLE 139	

WT1_PIG STANDARD: PRT: 449 AA.

AC 062651.

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE WILMS' TUMOR PROTEIN HOMOLOG.

GN WT1.

OS Sus scrofa (Pig)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-LMD: TISSUE-KIDNEY;

RX MEDLINE-96267201; PubMed-9602131;

RA Tsutsumi N., Oda H., Nakatsuru Y., Imai Y., Zhang S., Ueno Y., Ishikawa T.;

RT "CDNA cloning and developmental expression of the porcine homologue of WT1.";

RT Gene 211:215-220(1998).

CC -1- FUNCTION: POTENTIAL ROLE IN TRANSCRIPTIONAL REGULATION. RECOGNIZES AND BINDS TO THE DNA SEQUENCE 5'-GGCCCCGC-3'.

CC -1- SUBCELLULAR LOCATION: NUCLEAR.

CC -1- ALTERNATIVE PRODUCTS: TWO ALTERNATIVE SPLICE SITES EXISTS.

CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING KIDNEY DEVELOPMENT.

CC -1- SIMILARITY: BELONGS TO THE EGR FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.

CC -----

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CC -----

CC EMBL: AB010969; BAA28147.1; -

DR INTERPRO: IPR000822; -

DR INTERPRO: IPR000976; -

DR Pfam: PF00096; zf-C2H2; 4.

DR PRINTS: PR00048; ZINC_FINGER.

DR PRINTS: PR00049; WILMTUMOR.

DR PROSITE: PS00028; ZINC_FINGER_C2H2; 4.

KW Zinc-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein; Transcription regulation; Alternative splicing; Anti-oncogene.

K1 DOMAIN 28 83 PRO-RICH.

FT 323 438 ZINC FINGERS.

FT 323 347 C2H2-TYPE.

FT 323 377 C2H2-TYPE.

FT 353 377 C2H2-TYPE.

FT 383 405 C2H2-TYPE.

FT 414 438 C2H2-TYPE.

FT 249 265 MISSING (IN ISOFORM 2 AND ISOFORM 3) (BY SIMILARITY).

FT VANSPLIC 407 409 MISSING (IN ISOFORM 2 AND ISOFORM 4) (BY SIMILARITY).

FT SEQUENCE 449 AA; 49166 MW; 9C3E557B9F5A7B3 CRC64;

SO

QY 1 PSQASSGOARMPNAPYLPSCLE 23

DB 117 PSQASSGOARMPNAPYLPSCLE 139

Query Match 100.0%; Score 123; DB 1; Length 449;

Best Local Similarity 100.0%; Pred. No. 1,4e-11;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5

9KD_HUMAN STANDARD: PRT: 82 AA.

AC P13994.

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 01-JAN-1990 (Rel. 13, Last annotation update)

DE 9 KDA PROTEIN.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-FIBROBLAST;

RX MEDLINE-89078418; PubMed-3203696;

RA Lammers R., Gross G., Mayr U., Collins J.;

RT "Alternative mechanisms for gene activation induced by poly(rl).poly(rc) and Newcastle disease virus.";

RT Eur. J. Biochem. 178:93-99(1988).

CC -1- INDUCTION: BY POLY(RI), POLY(RC) AND NEWCASTLE DISEASE VIRUS.

CC -----

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CC -----

CC EMBL: X13956; CAA32138.1; -

DR PIR: S02660; S02660.

DR PIR: S02660; S02660.

SO SEQUENCE 82 AA; 8594 MW; 9B4A1552A489652 CRC64;

QY 1 PSQASSGOARMPNAPYLPSCLE 23

DB 23 PLEASSTRARFPCLPLYACPE 45

Query Match 42.3%; Score 52; DB 1; Length 82;

Best Local Similarity 47.8%; Pred. No. 0.19;

Matches 11; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

RESULT 6

YD03_YEAST STANDARD: PRT: 885 AA.

AC Q06639;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE PUTATIVE 101.7 KDA TRANSCRIPTIONAL REGULATORY PROTEIN IN PROI-CPRS INTERGENIC REGION.

GN YDR303C OR D9740.13.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-S288C / AB972;

RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z., Ravella A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D., Johnston L., Langston Y., Latreille P., Le T., Mardis E., Meneses S., Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L., Tach A., Trevasakis E., Vignati D., Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R.;

RT Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).

CC -1- SIMILARITY: CONTAINS A ZN(2)-CYS(6), FUNGAL-TYPE BINUCLEAR CLUSTER DOMAIN.

CC -----

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CC -----


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RL J. Biol. Chem. 268:22305-22312(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-SPLEEN;
RA MEDLINE-94307727; PubMed-7518410;
RA Kou K., Jenkins N.A., Gilbert D.J., Copeland N.G., Rotwein P.;
RA "Organization, expression, and chromosomal location of the mouse
RA insulin-like growth factor binding protein 5 gene."
RA Genomics 20:412-418(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-KIDNEY;
RA MEDLINE-95121750; PubMed-7529732;
RA Schuller A.G.P., Groffen C., van Neck J.W., Zwartthoff E.C.,
RA Drop S.L.S.;
RA "cDNA cloning and mRNA expression of the six mouse insulin-like
RA growth factor binding proteins."
RL Mol. Cell. Endocrinol. 104:57-66(1994).
CC -1- FUNCTION: IGF-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFs
CC AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH
CC PROMOTING EFFECTS OF THE IGFs ON CELL CULTURE. THEY ALTER THE
CC INTERACTION OF IGFs WITH THEIR CELL SURFACE RECEPTORS.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN KIDNEY, UTERUS AND
CC GASTROCNEMIUS MUSCLE.
CC -1- SIMILARITY: CONTAINS 1 THYROGLOBULIN TYPE-I DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
CC PROTEIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch)
CC -----
DR EMBL: L12447; AAC37636.1; -
DR EMBL: U02025; AAC01750.1; -
DR EMBL: U02023; AAC01750.1; JOINED.
DR EMBL: U02027; AAC01750.1; JOINED.
DR EMBL: U02024; AAC01750.1; JOINED.
DR EMBL: X81583; CA57273.1; -
DR MGD: MGI:96440; IGFBP5.
DR INTERPRO: IPR000716; -
DR INTERPRO: IPR000667; -
DR PFAM: PF00219; IGFBP_1.
DR PFAM: PF00086; lthyroglobulin_1; 1.
DR PROSITE: PS00222; IGF_BINDING; 1.
DR PROSITE: PS00484; THYROGLOBULIN_1; 1.
KW Growth factor binding; Signal.
FT SIGNAL 1 19
FT CHAIN 20 271
FT DOMAIN 214 262
FT CONFLICT 112 112 MISSING (IN REF. 2).
SQ SEQUENCE 271 AA; 30372 MW; F55A58729861F6F0 CRC64;

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Query Match          38.28; Score 47; DB 1; Length 271;
Best Local Similarity 47.48; Pred. No. 3.8;
Matches 9; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

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QY 3 QASSGQARMPNAPYLPSG 21
DB 200 QELKASPRMVPRAVYLPLNC 218

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RESULT 9
ID IBP5_PIG STANDARD; PRT; 271 AA.
AC Q28985;
DT 01-NOV-1997 (Rel. 35, Created)

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DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 5 PRECURSOR (IGFBP-5)
DE (IBP-5) (IGF-BINDING PROTEIN 5).
GN IGFBP5.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Sulina; Suidae; Sus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SKELETAL MUSCLE;
RA MEDLINE-96136309; PubMed-8573141;
RA White M.E., Diaz R., Hathaway M.R., Mickelson J., Dayton W.R.;
RA "Molecular cloning and sequence analysis of the porcine insulin-like
RA growth factor binding protein-5 complementary deoxyribonucleic
RA acid."
RL Biochem. Biophys. Res. Commun. 218:248-253(1996).
CC -1- FUNCTION: IGF-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFs
CC AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH
CC PROMOTING EFFECTS OF THE IGFs ON CELL CULTURE. THEY ALTER THE
CC INTERACTION OF IGFs WITH THEIR CELL SURFACE RECEPTORS.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: CONTAINS 1 THYROGLOBULIN TYPE-I DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
CC PROTEIN FAMILY.
CC -----
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CC -----
DR EMBL: U41340; AAA87859.1; -
DR INTERPRO: IPR000716; -
DR INTERPRO: IPR000667; -
DR PFAM: PF00219; IGFBP_1.
DR PFAM: PF00086; lthyroglobulin_1; 1.
DR PROSITE: PS00222; IGF_BINDING; 1.
DR PROSITE: PS00484; THYROGLOBULIN_1; 1.
KW Growth factor binding; Signal.
FT SIGNAL 1 19
FT CHAIN 20 271
FT DOMAIN 214 262
FT CONFLICT 112 112 MISSING (IN REF. 2).
SQ SEQUENCE 271 AA; 30323 MW; 95C254E95DC4EDBD CRC64;

```

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Query Match          38.28; Score 47; DB 1; Length 271;
Best Local Similarity 47.48; Pred. No. 3.8;
Matches 9; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

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QY 3 QASSGQARMPNAPYLPSG 21
DB 200 QELKASPRMVPRAVYLPLNC 218

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RESULT 10
ID IBP5_RAT STANDARD; PRT; 271 AA.
AC P24594;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 5 PRECURSOR (IGFBP-5)
DE (IBP-5) (IGF-BINDING PROTEIN 5).
GN IGFBP5 OR IGFBP-5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 20-53.

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DR PIR: JH0391; JH0391.
 DR PIR: B40403; B40403.
 DR PIR: PH0143; PH0143.
 DR PDB: 1BOE: 16-DEC-98.
 DR MIM: 146734; -.
 DR INTERPRO: IPR000716; -.
 DR INTERPRO: IPR000867; -.
 DR PFAM: PF00219; IGFBP_1.
 DR PFAM: PF00086; thyroglobulin_1.
 DR PROSITE: PS00222; IGF BINDING: 1.
 DR PROSITE: PS00484; THYROGLOBULIN_1.
 DR Growth factor binding; Signal: 3D-structure.
 DR SIGNAL: 20
 FT CHAIN 21 272
 FT INSULIN-LIKE GROWTH FACTOR BINDING
 FT PROTEIN 5.
 SO DOMAIN 215 263 THYROGLOBULIN TYPE I.
 SEQUENCE 272 AA; 30570 MW; 0A7AD37C6EEA3A61 CRC64;

Query Match 38.2%; Score 47; DB 1; Length 272;
 Best Local Similarity 47.4%; Pred. No. 3.8;
 Matches 9; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

OY 3 QASSGQARFNPAPYLPS 21
 Db 201 QELKASPRMVPRAVYLPC 219

RESULT 12
 SYK_STRCO
 ID SYK_STRCO STANDARD; PRT; 545 AA.
 AC G9X895;
 DT 01-OCF-2000 (Rel. 40, Created)
 DT 01-OCF-2000 (Rel. 40, Last sequence update)
 DT 01-OCF-2000 (Rel. 40, Last annotation update)
 DE LYSYL-TRNA SYNTHETASE (EC 6.1.1.6) (LYSINE--TRNA LIGASE) (LYSRS)
 DE (FRAGMENT).
 GN LYS OR SCE15.20C.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycetaceae; Streptomyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Murphy L., Harris D., Bentley S.D., Parkhill J., Barrell B.G.,
 RA Rajandream M.A.;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + L-LYSINE + TRNA(LYS) -> AMP +
 CC PYROPHOSPHATE + L-LYSYL-TRNA(LYS).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: AL049707; CAB41289.1; -
 DR PFAM: PF01921; tRNA-synt_1f_1;
 DR PROSITE: PS00178; AA-TRNA_LIGASE_I; 1.
 KW Aminoacyl-TRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
 FT NON_TER 1 1
 FT SIMILAR 8 16 "HIGH" REGION.
 FT SIMILAR 290 294 "KMSK" REGION.
 SO SEQUENCE 545 AA; 59738 MW; A9F962ADB028A64 CRC64;

Query Match 37.4%; Score 46; DB 1; Length 545;
 Best Local Similarity 52.9%; Pred. No. 11;
 Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 5 SSGQARFNPAPYLPS 21
 Db 173 SSGAGYFPYKPYCGNC 189

RESULT 13
 GLI_CHICK
 ID GLI_CHICK STANDARD; PRT; 556 AA.
 AC P55878;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE ZINC FINGER PROTEIN GLI1 (GLI) (FRAGMENT).
 DE GLI1 OR GLI.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97105842; PubMed-8948590;
 RA Marigo V., Johnson R.L., Vortkamp A., Tabin C.J.;
 RT "Sonic hedgehog differentially regulates expression of GLI and GLI3
 RT during limb development.";
 RL Dev. Biol. 180:273-283(1996).
 CC -1- FUNCTION: MAY REGULATE THE TRANSCRIPTION OF SPECIFIC GENES DURING
 CC NORMAL DEVELOPMENT. MAY PLAY A ROLE IN CRANIOFACIAL DEVELOPMENT
 CC AND DIGITAL DEVELOPMENT, AS WELL AS DEVELOPMENT OF THE CENTRAL
 CC NERVOUS SYSTEM AND GASTROINTESTINAL TRACT. IMPLICATED IN THE
 CC TRANSDUCTION OF SHH SIGNAL (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- SIMILARITY: BELONGS TO THE GLI FAMILY OF C2H2-TYPE ZINC-FINGER
 CC PROTEINS.
 CC -----
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 CC -----
 CC EMBL: U60762; AAB51659.1; -
 DR HSSP: P08151; 2G1I.
 DR INTERPRO: IPR000822; -
 DR PFAM: PF00096; Zf-C2H2; 5.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2; 4.
 KW Zinc-finger; Metal-binding; DNA-binding; Transcription regulation;
 KW Nuclear protein; Repeat.
 FT DOMAIN 247 399
 FT ZN_FING 247 399 ZINC FINGERS.
 FT ZN_FING 247 272 C2H2-TYPE.
 FT ZN_FING 280 307 C2H2-TYPE.
 FT ZN_FING 313 337 C2H2-TYPE.
 FT ZN_FING 343 368 C2H2-TYPE.
 FT ZN_FING 374 399 C2H2-TYPE.
 FT NON_TER 556 556
 SO SEQUENCE 556 AA; 60215 MW; 722D2A5A1CA4D98 CRC64;

Query Match 37.4%; Score 46; DB 1; Length 556;
 Best Local Similarity 38.1%; Pred. No. 11;
 Matches 8; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

OY 1 PSQASSGQARFNPAPYLPS 21
 Db 139 PGQOQKGGOLFSTPLPLPC 159

RESULT 14
 KSEL_ECOLI
 ID KSEL_ECOLI STANDARD; PRT; 382 AA.
 AC P42501;

```

DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE CAPSULE POLYSACCHARIDE EXPORT INNER-MEMBRANE PROTEIN KPSE.
GN KPSE.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-K1;
RX MEDLINE=94075243; PubMed=8253690;
RA Cieslewicz M.V., Steenbergen S.M., Vint E.R.;
RT Cloning, sequencing, expression, and complementation analysis of the
RT Escherichia coli K1 kps region 1 gene, kpse, and identification of an
RT upstream open reading frame encoding a protein with homology to
RT Guto.
RT J. Bacteriol. 175:8018-8023(1993).
CC -1- FUNCTION: INVOLVED IN THE TRANSLLOCATION OF THE POLYSIALIC ACID
CC CAPSULE.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
CC (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE BEXC/CTRB/KPSE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L19929; AAB51624.1; ALT_INIT.
KW Polysaccharide transport; Transport; Transmembrane; Inner membrane.
FT TRANSMEM 28 48 POTENTIAL.
FT TRANSMEM 357 377 POTENTIAL.
SQ SEQUENCE 382 AA; 43049 MW; 05D25E12BD86F4B5 CRC64;

Query Match 36.6%; Score 45; DB 1; Length 382;
Best Local Similarity 57.1%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 8 QARMPNAPYLPSC 21
DB 345 QESSFPNIPYLAC 358

RESULT 15
KSES_ECOLI STANDARD; PRT; 382 AA.
AC P42214;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CAPSULE POLYSACCHARIDE EXPORT INNER-MEMBRANE PROTEIN KPSE.
GN KPSE.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-K5;
RX MEDLINE=9338530; PubMed=8397187;
RA Pazhani C., Rosenow C., Boulnois G.J., Bronner D., Jann K.,
RA Roberts I.S.;
RT Molecular analysis of region 1 of the Escherichia coli K5 antigen
RT gene cluster: a region encoding proteins involved in cell surface
RT expression of capsular polysaccharide.
RL J. Bacteriol. 175:5978-5983(1993).
CC -1- FUNCTION: INVOLVED IN THE TRANSLLOCATION OF THE POLYSIALIC ACID
CC CAPSULE.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE

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CC (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE BEXC/CTRB/KPSE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X74567; CAA52655.1;
KW Polysaccharide transport; Transport; Transmembrane; Inner membrane.
FT TRANSMEM 28 48 POTENTIAL.
FT TRANSMEM 357 377 POTENTIAL.
SQ SEQUENCE 382 AA; 43044 MW; 44E9508484DC05B2 CRC64;

Query Match 36.6%; Score 45; DB 1; Length 382;
Best Local Similarity 57.1%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 8 QARMPNAPYLPSC 21
DB 345 QESSFPNIPYLAC 358

```

Search completed: April 11, 2001, 14:03:53
Job time: 114 sec

0.0

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 11, 2001, 13:53:45 ; Search time 14.03 Seconds

(without alignments)
111.313 Million cell updates/sec

Title: US-09-164-223-2

Perfect score: 123

Sequence: 1 PSQASSGQARMFPNAPLPSCLE 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq Length: 0

Maximum DB seq Length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 66:*

2: PIR1:*

3: PIR2:*

4: PIR3:*

5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	123	100.0	448	2	S33926
2	123	100.0	449	2	A38080
3	123	100.0	449	2	A39692
4	103	83.7	410	2	JC5046
5	52	42.3	82	2	S02660
6	49	39.8	634	2	E82999
7	49	39.8	885	2	S61189
8	48	39.0	188	2	I79500
9	48	39.0	188	2	JU0451
10	48	39.0	188	2	I59116
11	48	39.0	188	2	A29867
12	48	39.0	600	2	D83286
13	48	39.0	618	2	S68450
14	48	39.0	778	2	TI7679
15	47	38.2	271	2	JC4584
16	47	38.2	271	2	I48604
17	47	38.2	271	2	JC1463
18	47	38.2	272	2	A53748
19	47	38.2	815	2	B30843
20	47	38.2	815	2	JN0689
21	46	37.4	830	2	S15720
22	46	37.4	545	2	T36123
23	46	37.4	606	2	T45560
24	46	37.4	955	2	T00247
25	45.5	37.0	704	2	T24517
26	45	36.6	381	2	A54415
27	45	36.6	382	2	A48492
28	45	36.6	484	2	JC7350
29	45	36.6	488	2	T33739

30	44	35.8	292	2	G64695	conserved hypothet
31	44	35.8	292	2	A71824	probable ribonucle
32	44	35.8	376	2	T46097	hypothetical prote
33	44	35.8	393	2	T20268	hypothetical prote
34	44	35.8	449	2	JC5117	translation elonga
35	44	35.8	472	2	T04855	hypothetical prote
36	44	35.8	590	2	T11098	NADH dehydrogenase
37	44	35.8	602	2	S47880	probable outer mem
38	44	35.8	615	2	A82025	NEIL protein - yea
39	44	35.8	726	2	S67044	melanotransferrin
40	44	35.8	738	1	TFHUM	hypothetical prote
41	44	35.8	1286	2	B71413	epidermal growth f
42	43.5	35.4	188	2	A39787	epidermal growth f
43	43.5	35.4	188	2	A30362	glyceroldehyde-3-P
44	43.5	35.4	337	1	JT0286	DNA-directed DNA p
45	43.5	35.4	832	2	S67505	

ALIGNMENTS

RESULT 1
S33926
WILMS' tumor protein WT1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 10-May-1996
C:Accession: S33926
R:Sharma, P. M., Yang, X.; Bowman, M.; Roberts, V.; Sukumar, S.
Cancer Res. 52, 6407-6412, 1992
A:Title: Molecular cloning of rat WILMS' tumor complementary DNA and a study of messe
A:Reference number: S33926; MUID:93046155
A:Accession: S33926
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-448 <SHA>
A:Cross-references: EMBL:X69716
C:Genetics:
A:Gene: WT1
C:Keywords: tumor suppressor

Query Match 100.0%; Score 123; DB 2; Length 448;
Best Local Similarity 100.0%; Pred. No. 2.4e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PSQASSGQARMFPNAPLPSCLE 23
DB 116 PSQASSGQARMFPNAPLPSCLE 138
RESULT 2
A38080
WILMS tumor susceptibility protein WT1 - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Jun-2000
C:Accession: A38080; S08273; A34673; I38504; I52811; I56315; A56411; S26286
R:Gessler, M.; Konig, A.; Bruns, G.A.
Genomics 12, 807-813, 1992
A:Title: The genomic organization and expression of the WT1 gene.
A:Reference number: A38080; MUID:92241883
A:Accession: A38080
A:Molecule type: DNA
A:Residues: 1-449 <GES1>
A:Cross-references: GB:X61631; GB:S99414; NID:937981; PIDN:CAA43819.1; PID:9825731
A>Note: it is uncertain whether Met-1 is the initiator or whether translation is init
A>Note: Sequence extracted from NCBI backbone (NCBIN:99414, NCBIN:99422, NCBIN:99479,
R:Gessler, M.; Poustka, A.; Cavenee, W.; Neve, R.L.; Orkin, S.H.; Bruns, G.A.P.
Nature 343, 774-778, 1990
A:Title: Homozygous deletion in WILMS tumours of a zinc-finger gene identified by chr
A:Reference number: S08273; MUID:90158822
A:Accession: S08273
A:Molecule type: mRNA

RESULT 6
 E82999
 probable beta-ketolactam synthase PA5174 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 15-Sep-2000
 C:Accession: E82999
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Berman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, L.; Lory, S.; Olson, M.V.
 .: Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
 A:Reference number: A82950
 A:Accession: E82999
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-634 <STO>
 A:Cross-references: GB:AE004930; GB:AE004091; NID:g9951472; PIDN:AAG08559.1; GSPDB:GN001
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA5174

Query Match 39.8%; Score 49; DB 2; Length 634;
 Best Local Similarity 47.8%; Pred. No. 9.5;
 Matches 11; Conservative 3; Mismatches 5; Indels 4; Gaps 1;

OY 5 SSGQRMF---PNAPYLPSCLE 23
 :|||||: 111111:
 Db 296 TSGQARVIVGNSEAPILPEICIE 318

RESULT 7
 S61189
 probable membrane protein YDR303c - Yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein D9740.13
 C:Species: Saccharomyces cerevisiae
 C:Date: 23-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 29-Oct-1999
 C:Accession: S61189
 R:Diag, H.
 Submitted to the EMBL Data Library, June 1995
 A:Description: The sequence of S. cerevisiae cosmid 9740.
 A:Reference number: S61159
 A:Accession: S61189
 A:Molecule type: DNA
 A:Residues: 1-885 <DIN>
 A:Cross-references: EMBL:U28374; NID:g849207; PIDN:AAB64739.1; PID:g849220; GSPDB:GN0000
 C:Genetics:
 A:Gene: MIPS:YDR303c
 A:Map position: 4R
 C:Superfamily: unassigned GAL4-type zinc cluster proteins; GAL4 zinc binuclear cluster
 C:Keywords: transmembrane protein
 F:9-47/Domain: GAL4 zinc binuclear cluster homology <GAL4>
 F:422-438/Domain: transmembrane #status predicted <TM1>
 F:699-715/Domain: transmembrane #status predicted <TM2>

Query Match 39.8%; Score 49; DB 2; Length 885;
 Best Local Similarity 50.0%; Pred. No. 14;
 Matches 10; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

OY 1 PSQASSGQARMPNAPYLP 20
 ||:|||||: 111111:
 Db 53 PSSSSSNTROYVANGPIYLS 72

RESULT 8
 I79500
 myc protein - human
 C:Species: Homo sapiens (man)
 C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 05-Nov-1999
 C:Accession: I79500

R:Finer, S.N.; Nishikura, K.; Finger, L.R.; Haluska, F.G.; Finan, J.; Nowell, P.C.;
 Proc. Natl. Acad. Sci. U.S.A. 85, 3052-3056, 1988
 A:Title: Sequence analysis of the MYC oncogene involved in the t(8;14)(q24;q11) chrom
 A:Reference number: I59116; MUID:88203638
 A:Accession: I79500
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: DNA
 A:Residues: 1-188 <RES>
 A:Cross-references: GB:J03253; NID:g188976; PIDN:AAA59887.1; PID:g188977

Query Match 39.0%; Score 48; DB 2; Length 188;
 Best Local Similarity 72.7%; Pred. No. 3.8;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 13 PNAPYLPSCLE 23
 |:||||||| 32
 Db 22 PGRPWLPSCLE 32

RESULT 9
 J00451
 hypothetical 21K protein (c-myc 5' region) - chimpanzee
 C:Species: Pan troglodytes (chimpanzee)
 C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jul-2000
 C:Accession: J00451
 R:Argant, C.; Rigole, M.; Eladadi, M.E.; Galibert, F.
 Gene 97, 231-237, 1991
 A:Title: Cloning and nucleotide sequence of the chimpanzee c-myc gene.
 A:Reference number: J00449; MUID:91153652
 A:Accession: J00451
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-188 <ARG>
 A:Cross-references: GB:M38057; NID:g176652; PIDN:AAA72909.1; PID:g176655

Query Match 39.0%; Score 48; DB 2; Length 188;
 Best Local Similarity 72.7%; Pred. No. 3.8;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 13 PNAPYLPSCLE 23
 |:||||||| 32
 Db 22 PGRPWLPSCLE 32

RESULT 10
 I59116
 myc protein - human
 C:Species: Homo sapiens (man)
 C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 05-Nov-1999
 C:Accession: I59116
 R:Finer, S.N.; Nishikura, K.; Finger, L.R.; Haluska, F.G.; Finan, J.; Nowell, P.C.;
 Proc. Natl. Acad. Sci. U.S.A. 85, 3052-3056, 1988
 A:Title: Sequence analysis of the MYC oncogene involved in the t(8;14)(q24;q11) chrom
 A:Reference number: I59116; MUID:88203638
 A:Accession: I59116
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: DNA
 A:Residues: 1-188 <RES>
 A:Cross-references: GB:M20605; NID:g188974; PIDN:AAA59886.1; PID:g188975

Query Match 39.0%; Score 48; DB 2; Length 188;
 Best Local Similarity 72.7%; Pred. No. 3.8;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 13 PNAPYLPSCLE 23
 |:||||||| 32
 Db 22 PGRPWLPSCLE 32

RESULT 11

A29867
 hypothetical 20K protein (myc 5' region) (Burkitt lymphoma) - human
 C:Species: Homo sapiens (man)
 C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 18-Jun-1993
 C:Accession: A29867
 R:Shove, L.C.; Moore, R.C.A.; Erikson, J.; Croce, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 2824-2828, 1987
 A:Title: MYC oncogene involved in a t(8;22) chromosome translocation is not altered in
 A:Reference number: A29867; MUID:87204220
 A:Accession: A29867
 A:Molecule type: DNA
 A:Residues: 1-188 <SHO>

Query Match 39.0%; Score 48; DB 2; Length 188;
 Best Local Similarity 72.7%; Pred. No. 3.8;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 13 PNAFLPSCLE 23
 Db 22 PGRPLPSCLE 32

RESULT 12
 D83286
 hypothetical protein PA2886 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 15-Sep-2000
 C:Accession: D83286
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim,
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A:Reference number: A82950
 A:Accession: D83286
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-600 <STO>
 A:Cross-references: GB:AE004714; GB:AE004091; NID:g9948965; PIDN:AAG06274.1; GSPDB:GN001
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA2886

Query Match 39.0%; Score 48; DB 2; Length 600;
 Best Local Similarity 47.4%; Pred. No. 13;
 Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 OY 4 ASSGQARMPNAPYPSCL 22
 Db 125 AKSGIREMFSDAFPFMCV 143

RESULT 13
 S68450
 apoptosis inhibitor hiap-2 - human
 C:Species: Homo sapiens (man)
 C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000
 C:Accession: S68450
 R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farhanli,
 Nature 379, 349-353, 1996
 A:Title: Suppression of apoptosis in mammalian cells by NAIIP and a related family of IAP
 A:Reference number: A58182; MUID:96145249
 A:Accession: S68450
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-618 <LIS>
 A:Cross-references: EMBL:U45879; NID:g1184317; PIDN:AAC50372.1; PID:g1184318
 C:Function:
 A:Description: apoptotic suppressor
 C:Superfamily: RING finger homology
 C:Keywords: apoptosis; zinc finger

F:567-611/Domain: RING finger homology <RNG>

Query Match 39.0%; Score 48; DB 2; Length 618;
 Best Local Similarity 50.0%; Pred. No. 13;
 Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 OY 4 ASSGQARMPNAPYPSCL 23
 Db 236 AMSEHRRHFPNCPFLNSLE 255

RESULT 14
 T17679
 proline-rich protein A189R - Chlorella virus PBCV-1
 C:Species: Chlorella virus PBCV-1
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T17679
 R:Graves, M.V.; Van Etten, J.L.
 submitted to the EMBL Data Library, May 1999
 A:Reference number: Z18806
 A:Accession: T17679
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-778 <GRA>
 A:Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96557.1
 A:Experimental source: specific host Chlorella strain NC64A
 C:Genetics:
 A:Note: A189R

Query Match 39.0%; Score 48; DB 2; Length 778;
 Best Local Similarity 47.1%; Pred. No. 17;
 Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 OY 1 PSQASSGQARMPNAPY 17
 Db 170 PKQASGSGNGLFKRNF 186

RESULT 15
 JC4584
 insulin-like growth factor binding protein-5 precursor - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 10-Apr-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999
 C:Accession: JC4584; G23734
 R:White, M.E.; Diao, R.; Hathaway, M.R.; Mickelson, J.; Dayton, W.R.
 Biochem. Biophys. Res. Commun. 218, 248-253, 1996
 A:Title: Molecular cloning and sequence analysis of the porcine insulin-like growth f
 A:Reference number: JC4584; MUID:96136309
 A:Accession: JC4584
 A:Molecule type: mRNA
 A:Residues: 1-271 <WHI>
 A:Cross-references: GB:U41340; NID:g1173906; PIDN:AA87859.1; PID:g1173907
 A:Experimental source: skeletal muscle
 R:Shimasaki, S.; Gao, L.; Shimonaka, M.; Ling, N.
 Mol. Endocrinol. 5, 938-948, 1991
 A:Title: Isolation and molecular cloning of insulin-like growth factor-binding protei
 A:Reference number: A23734; MUID:92049376
 A:Accession: G23734
 A:Molecule type: protein
 A:Residues: 20-25, 'X', 27-28, 'X', 30-36, 'X', 38-39 <SHI>
 C:Comment: This protein has essential roles in the regulation and coordination of ins
 lays a role during myoblast proliferation and differentiation, and is important in th
 C:Superfamily: Insulin-like growth factor binding protein 1; thyroglobulin type I rep
 C:Keywords: differentiation; growth factor; skeletal muscle
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-271/Product: insulin-like growth factor binding protein-5 #status experimental <
 F:191-262/Domain: thyroglobulin type I repeat homology <THY1>

Query Match 38.2%; Score 47; DB 2; Length 271;
 Best Local Similarity 47.4%; Pred. No. 8;

Matches	9;	Conservative	1;	Mismatches	9;	Indels	0;	Gaps	0;
QY	3	QASSGQARMFPNAPYLPSG	21						
DB	200	QELKASPRMVPRAVYLLPNC	218						

Search completed: April 11, 2001, 14:02:32
 Job time: 527 sec

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OM protein - protein search, using sw model

Run on: April 11, 2001, 13:54:44 ; Search time 42.4 Seconds
(without alignments)
89.423 Million cell updates/sec

Title: US-09-164-223-2
123
Sequence: 1 PSQASSGQARMFPNAPYLPSCLE 23

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1027871 seqs, 16484993 residues
Total number of hits satisfying chosen parameters: 1027871

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending Patents-AA:*

1:	/cgn2_6/ptodata/2/paa/PCRTUS.COMB.pep.*
2:	/cgn2_6/ptodata/2/paa/US06.COMB.pep.*
3:	/cgn2_6/ptodata/2/paa/US07.COMB.pep.*
4:	/cgn2_6/ptodata/2/paa/US080.COMB.pep.*
5:	/cgn2_6/ptodata/2/paa/US081.COMB.pep.*
6:	/cgn2_6/ptodata/2/paa/US082.COMB.pep.*
7:	/cgn2_6/ptodata/2/paa/US083.COMB.pep.*
8:	/cgn2_6/ptodata/2/paa/US084.COMB.pep.*
9:	/cgn2_6/ptodata/2/paa/US085.COMB.pep.*
10:	/cgn2_6/ptodata/2/paa/US086.COMB.pep.*
11:	/cgn2_6/ptodata/2/paa/US087.COMB.pep.*
12:	/cgn2_6/ptodata/2/paa/US088.COMB.pep.*
13:	/cgn2_6/ptodata/2/paa/US089.COMB.pep.*
14:	/cgn2_6/ptodata/2/paa/US090.COMB.pep.*
15:	/cgn2_6/ptodata/2/paa/US091.COMB.pep.*
16:	/cgn2_6/ptodata/2/paa/US092.COMB.pep.*
17:	/cgn2_6/ptodata/2/paa/US093.COMB.pep.*
18:	/cgn2_6/ptodata/2/paa/US094.COMB.pep.*
19:	/cgn2_6/ptodata/2/paa/US095.COMB.pep.*
20:	/cgn2_6/ptodata/2/paa/US096.COMB.pep.*
21:	/cgn2_6/ptodata/2/paa/US097.COMB.pep.*
22:	/cgn2_6/ptodata/2/paa/US060.COMB.pep.*
23:	/cgn2_6/ptodata/1/paa/PCRTUS.COMB.pep.*
24:	/cgn2_6/ptodata/1/paa/US06.COMB.pep.*
25:	/cgn2_6/ptodata/1/paa/US07.COMB.pep.*
26:	/cgn2_6/ptodata/1/paa/US08.COMB.pep.*
27:	/cgn2_6/ptodata/1/paa/US09.COMB.pep.*
28:	/cgn2_6/ptodata/1/paa/US060.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	123	100.0	23	US-09-164-223-2	Sequence 2, Appli
2	123	100.0	23	US-09-164-223-3	Sequence 3, Appli
3	123	100.0	23	US-09-164-223-2	Sequence 2, Appli
4	123	100.0	23	US-09-164-223-3	Sequence 3, Appli
5	123	100.0	23	US-09-164-223-2	Sequence 2, Appli

6	123	100.0	23	US-09-164-223-3	Sequence 3, Appli
7	123	100.0	23	US-09-276-484-2	Sequence 2, Appli
8	123	100.0	23	US-09-276-484-3	Sequence 2, Appli
9	123	100.0	23	US-09-276-484A-2	Sequence 2, Appli
10	123	100.0	23	US-09-276-484A-3	Sequence 3, Appli
11	123	100.0	23	US-09-523-419-2	Sequence 2, Appli
12	123	100.0	23	US-09-523-419-3	Sequence 2, Appli
13	123	100.0	23	US-09-679-339-2	Sequence 2, Appli
14	123	100.0	23	US-09-679-339-3	Sequence 2, Appli
15	123	100.0	23	US-09-684-361-2	Sequence 2, Appli
16	123	100.0	23	US-09-684-361-3	Sequence 2, Appli
17	123	100.0	23	US-09-685-830-2	Sequence 2, Appli
18	123	100.0	23	US-09-685-830-3	Sequence 2, Appli
19	123	100.0	23	US-09-785-019-2	Sequence 2, Appli
20	123	100.0	23	US-09-785-019-3	Sequence 2, Appli
21	123	100.0	23	US-09-791-477-2	Sequence 2, Appli
22	123	100.0	23	US-09-791-477-3	Sequence 2, Appli
23	123	100.0	152	US-09-785-019-343	Sequence 343, App
24	123	100.0	154	US-09-037-179A-5	Sequence 5, Appli
25	123	100.0	154	US-09-037-179A-6	Sequence 6, Appli
26	123	100.0	154	US-09-785-019-335	Sequence 335, App
27	123	100.0	345	US-09-037-179A-2	Sequence 2, Appli
28	123	100.0	345	US-09-037-179B-2	Sequence 2, Appli
29	123	100.0	369	US-09-785-019-346	Sequence 346, App
30	123	100.0	410	US-09-785-019-333	Sequence 333, App
31	123	100.0	449	US-09-037-179A-4	Sequence 4, Appli
32	123	100.0	449	US-09-037-179A-6	Sequence 6, Appli
33	123	100.0	449	US-09-164-223-319	Sequence 319, App
34	123	100.0	449	US-09-164-223-320	Sequence 320, App
35	123	100.0	449	US-09-164-223-319	Sequence 319, App
36	123	100.0	449	US-09-164-223-320	Sequence 320, App
37	123	100.0	449	US-09-164-223-319	Sequence 319, App
38	123	100.0	449	US-09-164-223-320	Sequence 320, App
39	123	100.0	449	US-09-276-484-319	Sequence 319, App
40	123	100.0	449	US-09-276-484-320	Sequence 320, App
41	123	100.0	449	US-09-276-484A-319	Sequence 319, App
42	123	100.0	449	US-09-276-484A-320	Sequence 320, App
43	123	100.0	449	US-09-523-419-319	Sequence 319, App
44	123	100.0	449	US-09-523-419-320	Sequence 320, App
45	123	100.0	449	US-09-791-477-320	Sequence 320, App

ALIGNMENTS

RESULT 1
US-09-164-223-2
Sequence 2, Application US/09164223
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1 SPECIFIC IMMUNOTHERAPY
FILE REFERENCE: 210121.465
CURRENT APPLICATION NUMBER: US/09/164,223
CURRENT FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 320
SOFTWARE: Patentlin Ver. 2.0
SEQ ID NO 2
LENGTH: 23
TYPE: PRT
ORGANISM: Homo sapiens
US-09-164-223-2

Query Match 100.0%; Score 123; DB 15; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PSQASSGQARMFPNAPYLPSCLE 23
DB 1 PSQASSGQARMFPNAPYLPSCLE 23

```

RESULT 2
US-09-164-223-3
: Sequence 3, Application US/09164223
: GENERAL INFORMATION:
: APPLICANT: Gaiger, Alexander
: APPLICANT: Cheever, Martin A.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI SPECIFIC IMMUNOTHERAPY
: FILE REFERENCE: 210121.465
: CURRENT APPLICATION NUMBER: US/09/164,223
: CURRENT FILING DATE: 1998-09-30
: NUMBER OF SEQ ID NOS: 320
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 3
: LENGTH: 23
: TYPE: PR1
: ORGANISM: Mus musculus
US-09-164-223-3

```

Query Match	100.0%;	Score 123;	DB 15;	Length 23;
Best Local Similarity	100.0%;	Pred. No. 3.6e-11;		
Matches	23;	Conservative	0;	Mismatches
				Indels
				Gaps
QY	1	PSQASSQQAAMFNAPLPSCLE	23	
Db	1	PSQASSQQAAMFNAPLPSCLE	23	

```

RESULT 3
US-09-164-223-2
: Sequence 2, Application US/09164223A
: GENERAL INFORMATION:
: APPLICANT: Gaiger, Alexander
: APPLICANT: Cheever, Martin A.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTI SPECIFIC IMMUNOTHERAPY
: FILE REFERENCE: 210121.465
: CURRENT APPLICATION NUMBER: US/09/164,223A
: CURRENT FILING DATE: 1998-09-30
: NUMBER OF SEQ ID NOS: 320
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 23
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-164-223-2

```

	Query Match	100.0%	Score 123;	DB 15;	Length 23;
	Best Local Similarity	100.0%;	Pred. NO.3.6e-11;		
	Matches 23; Conservative 0;	Mismatches 0;			
QY	1 PSQAASSGAARMPNAPFLPSCLE 23				
Db	1 PSQAASSGAARMPNAPFLPSCLE 23				

```

RESULT      4
US-09-164-223-3
: Sequence 3, Application US/09164223A
: GENERAL INFORMATION:
: APPLICANT: Gaiger, Alexander
: APPLICANT: Cheever, Martin A.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1 SPECIFIC IMMUNOTHERAPY
: FILE REFERENCE: 210121.465
: CURRENT APPLICATION NUMBER: US/09/164,223A
: CURRENT FILING DATE: 1998-09-30
: NUMBER OF SEQ ID NOS: 320
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 3
: LENGTH: 23
: TYPE: PRT
: ORGANISM: Mus musculus
: US-09-164-223-3

```

	Query Match	Similarity	Score	DB	Length
	Best Local Similarity	100.0%	123	15	23
	Matches	Conservative	Pred.	No. 36-11	
	23	0	Mismatches	0	Gaps
Oy	1	PSOASSGOARMPNPAPSCLE	23		
Db	1	PSOASSGOARMPNPAPSCLE	23		

```

RESULT      5
US-09-164-223-2
: Sequence 2, Application US/09164223B
: GENERAL INFORMATION:
: APPLICANT: Gaiger, Alexander
: APPLICANT: Cheever, Martin A.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1 SPECIFIC IMMUNOTHERAPY
: FILE REFERENCE: 210121.465
: CURRENT APPLICATION NUMBER: US/09/164,223B
: CURRENT FILING DATE: 1998-09-30
: NUMBER OF SEQ ID NOS: 320
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 23
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-164-223-2

```

Query Match	100.0%;	Score 123;	DB 15;	Length 23;
Best Local Similarity	100.0%;	Pred. No. 3	6e-11;	
Matches 23;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	PSQASSGQARMPNAPYLPSCLE	23	
Db	1	PSQASSGQARMPNAPYLPSCLE	23	

```

RESULT 6
US-09-164-223-3
: Sequence 3, Application US/09164223B
: GENERAL INFORMATION:
: APPLICANT: Gaiger, Alexander
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR W11 SPECIFIC IMMUNOTHERAPY
: FILE REFERENCE: 210121.465
: CURRENT APPLICATION NUMBER: US/09/164,223B
: CURRENT FILING DATE: 1998-09-30
: NUMBER OF SEQ ID NOS: 320
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 3
: LENGTH: 23
: TYPE: PR1
: ORGANISM: Mus musculus
US-09-164-223-3

```

Query	100.0% Best Local Similarity	Score 123; Pred. NO. 3.6e-11;	DB 15; Matches 23;	Length 23; Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
1 PSQASSGQARMPNAPYLPSCLE	23						
1 PSQASSGQARMPNAPYLPSCLE	23						

```

RESULT 7
US-09-276-484-2
; Sequence 2, Application US/09276484
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.

```


;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
;; FILE REFERENCE: 210121.465C1
;; CURRENT APPLICATION NUMBER: US/09/276,484
;; CURRENT FILING DATE: 1999-03-25
;; NUMBER OF SEQ ID NOS: 326
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 2
;; LENGTH: 23
;; TYPE: PRT
;; ORGANISM: Homo sapien
US-09-276-484-2

Query Match 100.0%; Score 123; DB 16; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMFPNAPYLPSCLE 23
Db 1 PSQASSGQARMFPNAPYLPSCLE 23

RESULT 8
US-09-276-484-3
;; Sequence 3, Application US/09276484
;; GENERAL INFORMATION:
;; APPLICANT: Gaiger, Alexander
;; APPLICANT: Cheever, Martin A.
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
;; FILE REFERENCE: 210121.465C1
;; CURRENT APPLICATION NUMBER: US/09/276,484
;; CURRENT FILING DATE: 1999-03-25
;; NUMBER OF SEQ ID NOS: 326
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 3
;; LENGTH: 23
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-09-276-484-3

Query Match 100.0%; Score 123; DB 16; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMFPNAPYLPSCLE 23
Db 1 PSQASSGQARMFPNAPYLPSCLE 23

RESULT 9
US-09-276-484A-2
;; Sequence 2, Application US/09276484A
;; GENERAL INFORMATION:
;; APPLICANT: Gaiger, Alexander
;; APPLICANT: Cheever, Martin A.
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1 SPECIFIC
;; FILE REFERENCE: 210121.465C1
;; CURRENT APPLICATION NUMBER: US/09/276,484A
;; CURRENT FILING DATE: 1999-03-25
;; PRIOR APPLICATION NUMBER: US 09/164,223
;; PRIOR FILING DATE: 1999-09-30
;; NUMBER OF SEQ ID NOS: 326
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2
;; LENGTH: 23
;; TYPE: PRT
;; ORGANISM: Homo sapien
US-09-276-484A-2

Query Match 100.0%; Score 123; DB 16; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMFPNAPYLPSCLE 23
Db 1 PSQASSGQARMFPNAPYLPSCLE 23

RESULT 10
US-09-276-484A-3
;; Sequence 3, Application US/09276484A
;; GENERAL INFORMATION:
;; APPLICANT: Gaiger, Alexander
;; APPLICANT: Cheever, Martin A.
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1 SPECIFIC
;; FILE REFERENCE: 210121.465C1
;; CURRENT APPLICATION NUMBER: US/09/276,484A
;; CURRENT FILING DATE: 1999-03-25
;; PRIOR APPLICATION NUMBER: US 09/164,223
;; PRIOR FILING DATE: 1999-09-30
;; NUMBER OF SEQ ID NOS: 326
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 3
;; LENGTH: 23
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-09-276-484A-3

Query Match 100.0%; Score 123; DB 16; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMFPNAPYLPSCLE 23
Db 1 PSQASSGQARMFPNAPYLPSCLE 23

RESULT 11
US-09-523-419-2
;; Sequence 2, Application US/09523419
;; GENERAL INFORMATION:
;; APPLICANT: Hendrickson, Ronald C.
;; APPLICANT: Probst, Peter
;; APPLICANT: Reed, Steven G.
;; TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND THERAPY
;; FILE REFERENCE: 210121.492
;; CURRENT APPLICATION NUMBER: US/09/523,419
;; CURRENT FILING DATE: 2000-03-10
;; NUMBER OF SEQ ID NOS: 326
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 2
;; LENGTH: 23
;; TYPE: PRT
;; ORGANISM: Homo sapien
US-09-523-419-2

Query Match 100.0%; Score 123; DB 19; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMFPNAPYLPSCLE 23
Db 1 PSQASSGQARMFPNAPYLPSCLE 23

RESULT 12
US-09-523-419-3

```

; Sequence 3, Application US/09523419
; GENERAL INFORMATION:
; APPLICANT: Hendrickson, Ronald C.
; APPLICANT: Probst, Peter
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND THERAPY
; FILE REFERENCE: 210121.492
; CURRENT APPLICATION NUMBER: US/09/523,419
; CURRENT FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-523-419-3

```

```

Query Match          100.0%; Score 123; DB 19; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 PSQASSGQARMPNAPYLPSCLE 23
Db 1 PSQASSGQARMPNAPYLPSCLE 23

```

```

RESULT 13
US-09-679-339-2
; Sequence 2, Application US/09679339
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Xu, Jiangchun
; APPLICANT: Cheever, Martin
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.533
; CURRENT APPLICATION NUMBER: US/09/679,339
; CURRENT FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-679-339-2

```

```

Query Match          100.0%; Score 123; DB 20; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 PSQASSGQARMPNAPYLPSCLE 23
Db 1 PSQASSGQARMPNAPYLPSCLE 23

```

```

RESULT 14
US-09-679-339-3
; Sequence 3, Application US/09679339
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Xu, Jiangchun
; APPLICANT: Cheever, Martin
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.533
; CURRENT APPLICATION NUMBER: US/09/679,339
; CURRENT FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 357

```

```

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-679-339-3

```

```

Query Match          100.0%; Score 123; DB 20; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 PSQASSGQARMPNAPYLPSCLE 23
Db 1 PSQASSGQARMPNAPYLPSCLE 23

```

```

RESULT 15
US-09-684-361-2
; Sequence 2, Application US/09684361
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C2
; CURRENT APPLICATION NUMBER: US/09/684,361
; CURRENT FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-684-361-2

```

```

Query Match          100.0%; Score 123; DB 20; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 PSQASSGQARMPNAPYLPSCLE 23
Db 1 PSQASSGQARMPNAPYLPSCLE 23

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Job time: 512 sec

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Fri Apr 20 12:06:13 2001

us-09-164-223-2.rap

Fri Apr 20 12:06:12 2001

us-09-164-223-2.ra1

Page 1

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 11, 2001, 13:53:35 ; Search time 12.38 Seconds
(without alignments)
33.361 Million cell updates/sec

Title: US-09-164-223-2

Perfect score: 123

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Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents, AA:*

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3: /cgn2_6/ptodata/2/1aa/6_COMB.pep:*

4: /cgn2_6/ptodata/2/1aa/PCUTUS_COMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	123	100.0	154	1 US-08-102-942A-5	Sequence 5, Appl1
2	123	100.0	210	1 US-08-234-783-2	Sequence 2, Appl1
3	123	100.0	210	1 US-08-456-907-2	Sequence 2, Appl1
4	123	100.0	210	1 PCT-US95-05523-2	Sequence 2, Appl1
5	123	100.0	345	1 US-08-102-942A-2	Sequence 2, Appl1
6	123	100.0	429	1 US-08-234-783-4	Sequence 4, Appl1
7	123	100.0	429	1 US-08-456-907-4	Sequence 4, Appl1
8	123	100.0	429	1 PCT-US95-05523-4	Sequence 4, Appl1
9	123	100.0	449	1 US-08-102-942A-4	Sequence 4, Appl1
10	123	100.0	449	1 US-08-102-942A-6	Sequence 6, Appl1
11	123	100.0	449	1 PCT-US95-05922A-2	Sequence 2, Appl1
12	48	39.0	618	2 US-08-511-485-8	Sequence 8, Appl1
13	48	39.0	618	3 US-09-212-971-8	Sequence 8, Appl1
14	48	39.0	618	3 US-08-800-929A-8	Sequence 8, Appl1
15	48	39.0	618	3 PCT-US96-12860-2	Sequence 8, Appl1
16	47	38.2	186	1 US-08-698-551-6	Sequence 6, Appl1
17	47	38.2	186	1 US-08-602-228-6	Sequence 6, Appl1
18	47	38.2	186	2 US-08-649-341A-6	Sequence 6, Appl1
19	47	38.2	186	2 US-08-494-440B-6	Sequence 6, Appl1
20	47	38.2	186	2 US-08-533-901B-6	Sequence 6, Appl1
21	47	38.2	186	2 US-08-839-032A-6	Sequence 6, Appl1
22	47	38.2	186	2 US-08-839-031A-6	Sequence 6, Appl1
23	47	38.2	186	2 PCT-US95-12724-6	Sequence 6, Appl1
24	47	38.2	271	4 PCT-US92-01196-3	Sequence 8, Appl1
25	47	38.2	272	1 US-08-698-551-8	Sequence 8, Appl1
26	47	38.2	272	2 US-08-602-228-8	Sequence 8, Appl1
27	47	38.2	272	2 US-08-649-341A-8	Sequence 8, Appl1
28	47	38.2	272	2 US-08-494-440B-8	Sequence 8, Appl1

29	47	38.2	272	2 US-08-533-901B-8	Sequence 8, Appl1
30	47	38.2	272	2 US-08-839-032A-8	Sequence 8, Appl1
31	47	38.2	272	2 US-08-839-031A-8	Sequence 8, Appl1
32	47	38.2	272	4 PCT-US92-01196-4	Sequence 4, Appl1
33	47	38.2	272	4 PCT-US95-12724-8	Sequence 8, Appl1
34	44	35.8	717	5 5262177-5	Patent No. 5262177
35	44	35.8	719	2 US-08-520-933-3	Patent No. 5262177
36	44	35.8	738	5 5262177-2	Patent No. 5262177
37	43.5	35.4	94	1 US-08-208-008C-14	Sequence 14, Appl1
38	43.5	35.4	174	5 5256643-3	Patent No. 5256643
39	43.5	35.4	187	5 5256643-2	Patent No. 5256643
40	43.5	35.4	188	1 US-07-749-001-3	Sequence 3, Appl1
41	43.5	35.4	188	1 US-07-749-001-5	Sequence 5, Appl1
42	43.5	35.4	188	1 US-08-154-198-3	Sequence 3, Appl1
43	43.5	35.4	188	1 US-08-154-198-5	Sequence 5, Appl1
44	43.5	35.4	188	1 US-08-463-335-3	Sequence 3, Appl1
45	43.5	35.4	188	1 US-08-463-335-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1
US-08-102-942A-5
; Sequence 5, Application US/08102942A
; Patent No. 5726288
GENERAL INFORMATION:
; APPLICANT: Call, Katherine M.
; APPLICANT: Glaser, Thomas M.
; APPLICANT: Ito, Caryn Y.
; APPLICANT: Buckler, Alan J.
; APPLICANT: Pelletier, Jerry
; APPLICANT: Haber, Daniel A.
; APPLICANT: Rose, Elise A.
; APPLICANT: Housman, David E.
; APPLICANT: Bruening, Wendy
; APPLICANT: Darveau, Andre
; TITLE OF INVENTION: Localization and Characterization of the
; TITLE OF INVENTION: Wlms' Tumor Gene
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.
; ZIP: 02173
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/102,942A
; FILING DATE: 02-AUG-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
; NAME: Grahanan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-5194A2
TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 154 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-102-942A-5

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Query Match	100.0%	Score 123;	DB 1;	Length 210;
Best Local Similarity	100.0%	Pred. NO.7.6e-12;		
Matches 23; Conservative 0;		Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	PSOASSGOARMPNARYLPSCLE	23	
Db	128	PSOASSGOARMPNARYLPSCLE	150	

RESULT 3
 US-08-456-907-2
 : Sequence 2, Application US/08456907
 : Patent No. 5631142
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Herlyn, Meenhard
 :
 : APPLICANT: Morris, Jennifer
 :
 : APPLICANT: Rauscher III, Frank J.
 :
 : APPLICANT: Rodeck, Ulrich
 :
 : TITLE OF INVENTION: W11 Monoclonal Antibodies and Methods of
 : TITLE OF INVENTION: Use Therefor

```

1  NUMBER OF SEQUENCES: 7
2  CORRESPONDENCE ADDRESS:
3  ADDRESSEE: Howson and Howson
4  STREET: Spring House Corporate Cntr, PO Box 457
5  CITY: Spring House
6  STATE: Pennsylvania
7  COUNTRY: USA
8  ZIP: 19477
9
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Floppy disk
12 COMPUTER: IBM PC compatible
13 OPERATING SYSTEM: PC-DOS/MS-DOS
14 SOFTWARE: Patent Release #1.0, Version #1.25
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/08/456,907
17 FILING DATE:
18 CLASSIFICATION: 435
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: US 08/234,783
21 FILING DATE: 28-Apr-1994
22 ATTORNEY/AGENT INFORMATION:
23 NAME: Bak, Mary E.
24 REGISTRATION NUMBER: 31,215
25 REFERENCE/DOCKET NUMBER: WST48AUSA
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: 215-540-9200
28 TELEFAX: 215-540-5818
29 INFORMATION FOR SEQ ID NO: 2:
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 210 amino acids
32 TYPE: amino acid
33 TOPOLOGY: linear
34
35 MOLECULE TYPE: protein
36
37 US-08-456-907-2

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Query Match	100.0%;	Score 123;	DB 1;	Length 210;
Best Local Similarity	100.0%;	Prod. NO. 7.6e-12;		
Matches 22;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	PSQASSGQARNPAPNAPLPSCLE	23	
Db	128	PSQASSGQARNPAPNAPLPSCLE	150	

RESULT 4
PCT-US95-05523-2
Sequence 2, Application PC/US9505523
GENERAL INFORMATION:
APPLICANT: The Wistar Institute of Anatomy and Biology
TITLE OF INVENTION: WFI Monoclonal Antibodies and
TITLE OF INVENTION: Methods of Use Therefor
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
City: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05523
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/234,783
FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST48PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-05523-2

Query Match 100.0%; Score 123; DB 4; Length 210;
Best Local Similarity 100.0%; Pred. No. 7.6e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PSOASSGQARMFPNAPYLPSCLE 23
DB 128 PSOASSGQARMFPNAPYLPSCLE 150

RESULT 5
US-08-102-942A-2
Sequence 2, Application US/08102942A
Patent No. 5726288
GENERAL INFORMATION:
APPLICANT: Call, Katherine M.
APPLICANT: Glaser, Thomas M.
APPLICANT: Ito, Caryn Y.
APPLICANT: Buckler, Alan J.
APPLICANT: Pelletier, Jerry
APPLICANT: Haber, Daniel A.
APPLICANT: Rose, Elise A.
APPLICANT: Housman, David E.
APPLICANT: Bruening, Wendy
APPLICANT: Darveau, Andre
TITLE OF INVENTION: Localization and Characterization of the
TITLE OF INVENTION: Wilms' Tumor Gene
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/102,942A
FILING DATE: 02-AUG-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5194A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-102-942A-2

Query Match 100.0%; Score 123; DB 1; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PSOASSGQARMFPNAPYLPSCLE 23
DB 33 PSOASSGQARMFPNAPYLPSCLE 55

RESULT 6
US-08-234-783-4
Sequence 4, Application US/08234783
Patent No. 5622835
GENERAL INFORMATION:
APPLICANT: Herlyn, Meenhard
APPLICANT: Morris, Jennifer
APPLICANT: Rauscher III, Frank J.
APPLICANT: Rodeck, Ulrich
TITLE OF INVENTION: WT1 Monoclonal Antibodies and Methods of
TITLE OF INVENTION: Use Therefor
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/234,783
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST48USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 429 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-234-783-4

Query Match 100.0%; Score 123; DB 1; Length 429;
Best Local Similarity 100.0%; Pred. No. 1.7e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PSOASSGQARMFPNAPYLPSCLE 23
DB 117 PSOASSGQARMFPNAPYLPSCLE 139

RESULT 7
US-08-456-907-4
Sequence 4, Application US/08456907
Patent No. 5633142
GENERAL INFORMATION:
APPLICANT: Herlyn, Meenhard
APPLICANT: Morris, Jennifer
APPLICANT: Rauscher III, Frank J.
APPLICANT: Rodeck, Ulrich
TITLE OF INVENTION: WT1 Monoclonal Antibodies and Methods of

;; TITLE OF INVENTION: Use Therefor
;; NUMBER OF SEQUENCES: 7
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Howson and Howson
;; STREET: Spring House Corporate Cntr, PO Box 457
;; CITY: Spring House
;; STATE: Pennsylvania
;; COUNTRY: USA
;; ZIP: 19477
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/456,907
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/234,783
;; FILING DATE: 28-APR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bak, Mary E.
;; REGISTRATION NUMBER: 31,215
;; REFERENCE/DOCKET NUMBER: WST48AUSA
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-540-9200
;; TELEFAX: 215-540-5818
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 429 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-456-907-4

Query Match 100.0%; Score 123; DB 1; Length 429;
Best Local Similarity 100.0%; Pred. No. 1.7e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMPNAPLPSCLE 23
Db 117 PSQASSGQARMPNAPLPSCLE 139

RESULT 8
PCT-US95-05523-4
;; Sequence 4, Application PC/TUS9505523
;; GENERAL INFORMATION:
;; APPLICANT: The Wistar Institute of Anatomy and Biology
;; TITLE OF INVENTION: WTI Monoclonal Antibodies and
;; NUMBER OF SEQUENCES: 7
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Howson and Howson
;; STREET: Spring House Corporate Cntr, PO Box 457
;; CITY: Spring House
;; STATE: Pennsylvania
;; COUNTRY: USA
;; ZIP: 19477
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/05523
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/234,783
;; FILING DATE: 28-APR-1994

;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bak, Mary E.
;; REGISTRATION NUMBER: 31,215
;; REFERENCE/DOCKET NUMBER: WST48PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-540-9200
;; TELEFAX: 215-540-5818
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 429 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; PCT-US95-05523-4

Query Match 100.0%; Score 123; DB 4; Length 429;
Best Local Similarity 100.0%; Pred. No. 1.7e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMPNAPLPSCLE 23
Db 117 PSQASSGQARMPNAPLPSCLE 139

RESULT 9
US-08-102-942A-4
;; Sequence 4, Application US/08102942A
;; Patent No. 5726288
;; GENERAL INFORMATION:
;; APPLICANT: Call, Katherine M.
;; APPLICANT: Glaser, Thomas M.
;; APPLICANT: Ito, Caryn Y.
;; APPLICANT: Buckler, Alan J.
;; APPLICANT: Pelletier, Jerry
;; APPLICANT: Haber, Daniel A.
;; APPLICANT: Rose, Elise A.
;; APPLICANT: Housman, David E.
;; APPLICANT: Bruening, Wendy
;; APPLICANT: Darveau, Andre
;; TITLE OF INVENTION: Localization and Characterization of the
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
;; STREET: Two Millitia Drive
;; CITY: Lexington
;; STATE: Massachusetts
;; COUNTRY: U.S.
;; ZIP: 02173
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/102,942A
;; FILING DATE: 02-AUG-1993
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Granahan, Patricia
;; REGISTRATION NUMBER: 32,227
;; REFERENCE/DOCKET NUMBER: MIT-5194A2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-861-6240
;; TELEFAX: 617-861-9540
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 449 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-102-942A-4

Query Match 100.0%; Score 123; DB 1; Length 449;
Best Local Similarity 100.0%; Pred. No. 1.8e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMPNAPYLPSCLE 23
|||||
DB 117 PSQASSGQARMPNAPYLPSCLE 139

RESULT 10
US-08-102-942A-6
; Sequence 6, Application US/08102942A
; Patent No. 5726288

GENERAL INFORMATION:
APPLICANT: Call, Katherine M.
APPLICANT: Glaser, Thomas M.
APPLICANT: Ito, Caryn Y.
APPLICANT: Buckler, Alan J.
APPLICANT: Pelletier, Jerry
APPLICANT: Haber, Daniel A.
APPLICANT: Rose, Elise A.
APPLICANT: Housman, David E.
APPLICANT: Darveau, Andre
APPLICANT: Darveau, Wendy
TITLE OF INVENTION: Localization and Characterization of the
TITLE OF INVENTION: Wilms' Tumor Gene
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.
ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/102,942A
FILING DATE: 02-AUG-1993

CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5194A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-102-942A-6

Query Match 100.0%; Score 123; DB 1; Length 449;
Best Local Similarity 100.0%; Pred. No. 1.8e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMPNAPYLPSCLE 23
|||||
DB 117 PSQASSGQARMPNAPYLPSCLE 139

RESULT 11
PCT-US95-05922A-2

Sequence 2, Application PC/TUS9505922A
GENERAL INFORMATION:

APPLICANT: HE, ET AL.
TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05922A
FILING DATE: 11 MAY 1995
CLASSIFICATION:
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-292
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
PCT-US95-05922A-2

Query Match 39.0%; Score 48; DB 4; Length 438;
Best Local Similarity 50.0%; Pred. No. 7.1;
Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 4 ASSGQARMPNAPYLPSCLE 23
|||
DB 56 AMSEHRRHFPNCPLENSLE 75

RESULT 12
US-08-511-485-8
; Sequence 8, Application US/08511485
; Patent No. 5919912

GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/511,485
 FILING DATE: 04-AUG-1995
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 07540/002001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 618 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: both
 MOLECULE TYPE: protein
 US-08-511-485-8

Query Match 39.0%; Score 48; DB 2; Length 618;
 Best Local Similarity 50.0%; Pred. No. 10;
 Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 4 ASSGQARMPNAPYLPSCLE 23
 || |||||:|:|
 Db 236 AMSEHRRHFPNCPLFLENSLE 255

RESULT 13
 US-09-212-971-8
 Sequence 8, Application US/09212971B
 Patent No. 6107041
 GENERAL INFORMATION:
 APPLICANT: Korneluk, Robert G
 APPLICANT: Mackenzie, Alexander E
 APPLICANT: Liston, Peter
 APPLICANT: Baird, Stephen
 APPLICANT: Tsang, Benjamin K
 APPLICANT: Pratt, Christine
 TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
 TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
 TITLE OF INVENTION: DISEASE
 FILE REFERENCE: 07891/009002
 CURRENT APPLICATION NUMBER: US/09/212,971B
 EARLIER FILING DATE: 1998-12-16
 EARLIER APPLICATION NUMBER: 60/017,354
 EARLIER FILING DATE: 1996-04-26
 EARLIER APPLICATION NUMBER: 60/030,590
 EARLIER FILING DATE: 1996-11-14
 EARLIER APPLICATION NUMBER: 08/800,929
 EARLIER FILING DATE: 1997-02-13
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 8
 LENGTH: 618
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-212-971-8

Query Match 39.0%; Score 48; DB 3; Length 618;
 Best Local Similarity 50.0%; Pred. No. 10;
 Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 4 ASSGQARMPNAPYLPSCLE 23
 || |||||:|:|
 Db 236 AMSEHRRHFPNCPLFLENSLE 255

RESULT 14
 US-08-800-929A-8
 Sequence 8, Application US/08800929A
 Patent No. 613437
 GENERAL INFORMATION:
 APPLICANT: Korneluk, Robert G
 APPLICANT: Mackenzie, Alexander E
 APPLICANT: Liston, Peter
 APPLICANT: Baird, Stephen
 APPLICANT: Tsang, Benjamin K
 APPLICANT: Pratt, Christine
 TITLE OF INVENTION: DETECTION AND MODULATION OF
 TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERAT
 TITLE OF INVENTION: DISEASE
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Clark & Elbing LLP
 STREET: 176 Federal Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/800,929A
 FILING DATE: 13-FEB-1997
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/030,590
 FILING DATE: 14-NOV-1996
 APPLICATION NUMBER: 60/017,354
 FILING DATE: 26-APR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Bleker-Brady, Kristina
 REGISTRATION NUMBER:
 REFERENCE/DOCKET NUMBER: 07891/009001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-428-0200
 TELEFAX: 617-428-7045
 TELEX:
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 618 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-800-929A-8

Query Match 39.0%; Score 48; DB 3; Length 618;
 Best Local Similarity 50.0%; Pred. No. 10;
 Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 4 ASSGQARMPNAPYLPSCLE 23
 || |||||:|:|
 Db 236 AMSEHRRHFPNCPLFLENSLE 255

RESULT 15
 PCT-US96-12860-2
 Sequence 2, Application PC/TUS9612860
 GENERAL INFORMATION:
 APPLICANT: TUDARIK, INC.
 TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FLIER, HOBBACH, TEST, ALBRITTON & HERBERT
 STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/12860
 FILING DATE: 06 AUG 1996
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Brezner, David J.
 REGISTRATION NUMBER: 24,774
 REFERENCE/DOCKET NUMBER: A-62464/DJB
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415)781-1989
 TELEFAX: (415)398-3249
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 618 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US96-12860-2

Query Match 39.0%; Score 48; DB 4; Length 618;
 Best Local Similarity 50.0%; Pred. No. 10;
 Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 QY 4 ASSGQARMPFNAPYLPSCLE 23
 DB 236 AMSEHRRHFNCPLENSLE 255

Search completed: April 11, 2001, 14:02:12
 Job time: 517 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 11, 2001, 13:53:18 ; Search time 15.5 Seconds
(without alignments)
50.739 Million cell updates/sec

Title: US-09-164-223-2
Perfect score: 123
Sequence: 1 PSQASSGQARMPNAPLPSCLE 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq.36.*
1: /SIDSL/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDSL/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: /SIDSL/gcgdata/geneseq/geneseqp/AA1982.DAT:*
4: /SIDSL/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5: /SIDSL/gcgdata/geneseq/geneseqp/AA1984.DAT:*
6: /SIDSL/gcgdata/geneseq/geneseqp/AA1985.DAT:*
7: /SIDSL/gcgdata/geneseq/geneseqp/AA1986.DAT:*
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9: /SIDSL/gcgdata/geneseq/geneseqp/AA1988.DAT:*
10: /SIDSL/gcgdata/geneseq/geneseqp/AA1989.DAT:*
11: /SIDSL/gcgdata/geneseq/geneseqp/AA1990.DAT:*
12: /SIDSL/gcgdata/geneseq/geneseqp/AA1991.DAT:*
13: /SIDSL/gcgdata/geneseq/geneseqp/AA1992.DAT:*
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15: /SIDSL/gcgdata/geneseq/geneseqp/AA1994.DAT:*
16: /SIDSL/gcgdata/geneseq/geneseqp/AA1995.DAT:*
17: /SIDSL/gcgdata/geneseq/geneseqp/AA1996.DAT:*
18: /SIDSL/gcgdata/geneseq/geneseqp/AA1997.DAT:*
19: /SIDSL/gcgdata/geneseq/geneseqp/AA1998.DAT:*
20: /SIDSL/gcgdata/geneseq/geneseqp/AA1999.DAT:*
21: /SIDSL/gcgdata/geneseq/geneseqp/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	123	100.0	23	21	Y98502 Human WTI peptide
2	123	100.0	23	21	Y98503 Human WTI peptide
3	123	100.0	154	19	W47175 Wtlms' tumour poly
4	123	100.0	210	16	W47175 Wtlms' tumour anti
5	123	100.0	210	18	W22883 Wtlms' tumour prot
6	123	100.0	345	12	R12240 Wtlms' tumour gene
7	123	100.0	345	19	W47173 Wtlms' tumour poly
8	123	100.0	429	16	R85065 Wtlms' tumour WTI
9	123	100.0	449	21	W47176 Wtlms' tumour poly
10	123	100.0	449	21	Y98804 Human WTI protein
11	123	100.0	449	21	Y98805 Mouse WTI protein
12	123	100.0	449	21	Y80196 Mouse Wtlms' tumour

13	123	100.0	449	21	Y80197 Human Wtlms' tumour
14	55	44.7	9	21	Y98810 WTI related peptid
15	53	43.1	9	21	Y98809 WTI related peptid
16	52	42.3	9	21	Y98564 WTI derived immuno
17	52	42.3	9	21	Y98752 WTI derived immuno
18	52	42.3	9	21	Y98752 WTI derived immuno
19	52	42.3	9	21	Y98752 WTI derived immuno
20	51	41.5	9	21	Y94202 Human cytotoxic T
21	51	41.5	9	21	Y98670 WTI derived immuno
22	51	41.5	9	21	Y98670 WTI related peptid
23	51	41.5	9	21	Y98778 Human Wtlms' tumour
24	51	41.5	9	21	Y80200 WTI related peptid
25	51	41.5	9	21	Y98808 WTI derived immuno
26	49	39.8	9	21	Y98808 WTI derived immuno
27	48	39.0	9	21	Y98583 WTI related peptid
28	48	39.0	9	21	Y98697 WTI derived immuno
29	48	39.0	9	21	Y98754 Human IGFBP-5. Sy
30	48	39.0	272	13	R26995 Human inhibitor of
31	48	39.0	438	17	W04563 Human c-14p1. Hom
32	48	39.0	618	18	W19746 Human H1AP-2 prote
33	48	39.0	618	18	W19583 Human cellular inh
34	48	39.0	618	18	W13545 Insulin-like growth
35	48	39.0	618	19	W69296 Human insulin-like
36	48	39.0	618	20	Y33998 Human insulin-like
37	47	38.2	113	20	Y25508 Insulin like growth
38	47	38.2	186	17	R95328 Tumor necrosis fac
39	47	38.2	186	18	W3571 Rat IGFBP-5. Synt
40	47	38.2	271	13	R26994 IGFBP6. Synthetic
41	47	38.2	272	13	R25700 Human insulin-like
42	47	38.2	272	17	R55084 Insulin like growth
43	47	38.2	272	17	R95329 Insulin like growth
44	47	38.2	272	18	W35572 A human insulin-11
45	47	38.2	272	21	Y33969

ALIGNMENTS

RESULT 1	Y98502	standard; Peptide: 23 AA.
ID	Y98502:	
AC	Y98502:	
XX		
DT	31-JUN-2000 (first entry)	
XX		
DE	Human WTI peptide SEQ ID NO:2.	
XX		
XX		
KW	WT1; immunotherapy; immunogenic; malignant disease; cancer; leukaemia;	
KW	metastatic disease; mouse; human; Wtlms' tumour; immune response;	
KW	vaccine.	
XX		
OS	Homo sapiens.	
XX		
PN	W0200018795-A2.	
XX		
PD	06-APR-2000.	
XX		
PF	30-SEP-1999; 99WO-US22819.	
XX		
PR	30-SEP-1998; 98US-0164223.	
XX		
PR	25-MAR-1999; 99US-0276484.	
XX		
PA	(CORI-) CORIXA CORP.	
XX	(GALG/) GALGER A.	
XX		
PI	Gaiger A, Cheever M;	
XX		
DR	WPI; 2000-293107/25.	
XX		
PT	Novel polypeptides comprising an immunogenic portion of a native WTI	
XX	polypeptide, useful for inhibiting the development of malignant	
PT	diseases associated with WTI expression e.g. leukemia or cancer	
XX		
PT		

XX Claim 4: Page 46: 193pp: English.

CC The present invention describes polypeptides (I) comprising an
 CC immunogenic portion of a native Wilm's Tumour gene product polypeptide,
 CC WT1, (or variants of the immunogenic portion retaining the ability to
 CC react with WT1-specific antisera and/or T-cell lines or clones) and
 CC comprising 16 consecutive amino acids (aa) or less of a native WT1
 CC polypeptide. The polypeptides are useful therapeutically and to
 CC manufacture medicaments for enhancing/inducing an immune response in
 CC patients. The polypeptides, mimetics or polynucleotides can be included
 CC with a carrier/excipient in pharmaceutical compositions or with a
 CC non-specific immune response enhancer (e.g. an adjuvant or enhancer
 CC preferentially enhancing a T cell response) in vaccines. Pharmaceutical
 CC compositions and vaccines can be administered to human patients to
 CC enhance or induce an immune response specific for WT1 or a cell
 CC expressing WT1, useful to inhibit the development of malignant diseases
 CC associated with WT1 expression, e.g. leukemia (especially acute/chronic
 CC myeloid leukemia or acute lymphocytic leukemia) or cancer (especially
 CC breast, lung, thyroid or gastrointestinal cancer, or a melanoma). Y98501
 CC to Y98811 represent polypeptide sequences, and A13848 to A13862 represent
 CC PCR primers, used in the exemplification of the present invention.

XX Sequence 23 AA:

Query Match 100.0%; Score 123; DB 21; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.5e-13;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGOARFNPAPLPSCLE 23
 Db 1 psgassgqarmfpnaplp scale 23

RESULT 2
 Y98503 Y98503 standard; Peptide: 23 AA.

AC Y98503;

DT 31-JUL-2000 (first entry)

DE Mouse WT1 peptide SEQ ID NO:3.

XX WT1: immunotherapy; immunogenic; malignant disease; cancer; leukemia;
 KW metastatic disease; mouse; human; Wilm's tumour; immune response;
 KW vaccine.

OS Mus musculus.

PN WO200018795-A2.

PD 06-APR-2000.

XX 30-SEP-1999; 99WO-US22819.

XX 30-SEP-1998; 98US-0164223.

PR 25-MAR-1999; 99US-0276484.

PA (CORI-) CORIXA CORP.
 (GAIG/) GAIGER A.

PI Galger A, Cheever M;

DR WPI: 2000-293107/25.

XX Novel polypeptides comprising an immunogenic portion of a native WT1
 PT polypeptide, useful for inhibiting the development of malignant
 PT diseases associated with WT1 expression e.g. leukemia or cancer
 XX Example 3; Page 46; 193pp: English.

CC The present invention describes polypeptides (I) comprising an
 CC immunogenic portion of a native Wilm's Tumour gene product polypeptide,
 CC WT1, (or variants of the immunogenic portion retaining the ability to
 CC react with WT1-specific antisera and/or T-cell lines or clones) and
 CC comprising 16 consecutive amino acids (aa) or less of a native WT1
 CC polypeptide. The polypeptides are useful therapeutically and to
 CC manufacture medicaments for enhancing/inducing an immune response in
 CC patients. The polypeptides, mimetics or polynucleotides can be included
 CC with a carrier/excipient in pharmaceutical compositions or with a
 CC non-specific immune response enhancer (e.g. an adjuvant or enhancer
 CC preferentially enhancing a T cell response) in vaccines. Pharmaceutical
 CC compositions and vaccines can be administered to human patients to
 CC enhance or induce an immune response specific for WT1 or a cell
 CC expressing WT1, useful to inhibit the development of malignant diseases
 CC associated with WT1 expression, e.g. leukemia (especially acute/chronic
 CC myeloid leukemia or acute lymphocytic leukemia) or cancer (especially
 CC breast, lung, thyroid or gastrointestinal cancer, or a melanoma). Y98501
 CC to Y98811 represent polypeptide sequences, and A13848 to A13862 represent
 CC PCR primers, used in the exemplification of the present invention.

XX Sequence 23 AA:

Query Match 100.0%; Score 123; DB 21; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.5e-13;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGOARFNPAPLPSCLE 23
 Db 1 psgassgqarmfpnaplp scale 23

RESULT 3
 W47175 W47175 standard; Protein: 154 AA.

AC W47175;

DT 01-JUN-1998 (first entry)

DE Wilms' tumour polypeptide (WT33) proline and glutamine rich region.

XX Wilm's tumour; WT33; cancer treatment; antibody production; WAGR;

KW Denys-drash Syndrome; WT1.

XX Homo sapiens.

OS US5726288-A.

PN 10-MAR-1998.

PD 02-AUG-1993; 93US-0102942.

XX 02-AUG-1993; 93US-0102942.

PR 13-NOV-1989; 89US-0435780.

XX 13-NOV-1990; 90US-0614161.

PA (MASI) MASSACHUSETTS INSTR TECHNOLOGY.

PI Bruening W, Buckler AJ, Gall KM, Darveau A, Glaser TM,
 PI Haber DA, Housman DE, Ito CY, Pelletier J, Rose EA.

DR WPI: 1998-192828/17.

XX New Wilm's tumour polypeptide - useful for, e.g. cancer treatment
 PT and antibody production

XX Claim 2; Fig 4; 42pp: English.

XX This sequence represents the proline and glutamine rich region of a new
 CC Wilm's tumour (WT33) polypeptide. The Wilm's tumour gene (WT1) is
 CC associated with 11p3 locus on the human chromosome. This proline and
 CC glutamine rich region indicates that the Wilm's tumour polypeptide has

Query Match 100.0%; Score 123; DB 18; Length 210;
 Best Local Similarity 100.0%; Pred. No. 1.9e-12;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMPNAPYLPSCLE 23
 |||||||
 ,Db 128 psgassgqarmfnpaylpsele 150

RESULT 6

R12240
 ,ID R12240 standard; Protein; 345 AA.

AC R12240;

DT 15-AUG-1991 (first entry)

XX Wilm's tumour gene prod.

DE Wilm's tumour; monoclonal antibodies.

XX Homo sapiens.

OS Key Location/Qualifiers

FT Domain 3..156 /label= proline/glutamine rich region

FT Domain 216..226 /label= zinc finger domain 1

FT Domain 227..246 /label= zinc finger domain 2

FT Domain 247..276 /label= zinc finger domain 3

FT Domain 277..304 /label= zinc finger domain 4

PN W09107509-A.

PD 30-MAY-1991.

PF 13-NOV-1990; 90MO-US06629.

PR 13-NOV-1989; 89US-0435780.

PA (MAST) MASSACHUSETTS INST TECH.

PI Call KM, Glaser TM, Ito CY, Buckler AJ, Pelletier J;

PI Haber DA, Rose EA, Housman DE;

DR WPI; 1991-178117/24.

DR N-PSDB; Q12020.

PT Nucleotide sequence of human chromosome 11 band 13 Wilm's tumour

PS locus - used to diagnose, quantify and treat Wilm's tumours

XX Disclosure; fig 3; 67pp; English.

CC This polypeptide is encoded by the Wilm's tumour (WT) gene which
 CC maps to the 11p13 locus of human chromosome 11. It contains 4
 CC zinc finger binding domains and a proline/glutamine rich region
 CC and hence is thought to be involved in transcription regulation.
 CC using this WT protein and the DNA, probes and antibodies can be
 CC developed for diagnosing WT. Lesions similar to WT may also
 CC be detected.

SO Sequence 345 AA;

Query Match 100.0%; Score 123; DB 12; Length 345;

Best Local Similarity 100.0%; Pred. No. 3.3e-12;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMPNAPYLPSCLE 23
 |||||||

Db 33 psgassgqarmfnpaylpsele 55

RESULT 7

W47173
 ID W47173 standard; Protein; 345 AA.

AC W47173;

DT 01-JUN-1998 (first entry)

XX Wilm's tumour polypeptide (WT33).

DE Wilm's tumour; WT33; cancer treatment; antibody production; WAGR;

XX Denys-drash syndrome; WT1.

XX Homo sapiens.

OS Key Location/Qualifiers

FT Region 3..156 /note= "proline and glutamine rich region"

PN US5726288-A.

PD 10-MAR-1998.

PE 02-AUG-1993; 93US-0102942.

PR 02-AUG-1993; 93US-0102942.

PR 13-NOV-1989; 89US-0435780.

PR 13-NOV-1990; 90US-0614161.

XX (MAST) MASSACHUSETTS INST TECHNOLOGY.

XX Bruening W, Buckler AJ, Call KM, Darveau A, Glaser TM;

PI Haber DA, Housman DE, Ito CY, Pelletier J, Rose EA;

DR WPI; 1998-192828/17.

DR N-PSDB; V17060.

PT New Wilm's tumour polypeptide - useful for, e.g. cancer treatment

PS and antibody production

XX Claim 2; Fig 3; 42pp; English.

CC This is a new Wilm's tumour (WT33) polypeptide. The Wilm's tumour gene
 CC (WT1) is associated with 11p13 locus on the human chromosome. This
 CC polypeptide has a region rich in proline and glutamine (W47173)
 CC indicating that it has a role in transcription regulation. The
 CC polypeptide or immunogenic fragments of the polypeptide can be used to
 CC treat cancerous or precancerous conditions (especially Wilm's tumour), or
 CC to raise antibodies for diagnostic use. The product allow detection of
 CC risk of development of Wilm's tumour, e.g. in diseases such as WAGR and
 CC Denys-Drash syndrome, to be assessed prior to current methods of
 CC detection.

SO Sequence 345 AA;

Query Match 100.0%; Score 123; DB 19; Length 345;

Best Local Similarity 100.0%; Pred. No. 3.3e-12;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMPNAPYLPSCLE 23
 |||||||

Db 33 psgassgqarmfnpaylpsele 55

RESULT 8

R85065
 ID R85065 standard; Protein; 429 AA.

AC R85065;


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XX 02-FEB-1996 (first entry)
DT Wlms' tumour WT1 antigen.
DE Wlms' tumour WT1; monoclonal antibody; leukaemia.
XX Wlms' tumour; WT1; monoclonal antibody; leukaemia.
XX Homo sapiens.
XX WO9529995-A1.
XX 09-NOV-1995.
XX 25-APR-1995: 95WO-US05523.
XX 28-APR-1994: 94US-0234783.
XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.
XX Herlyn M, Morris J, Rauscher FJ, Rodeck U;
DR WPI; 1995-393072/50.
DR N-PSDB; R85065.
XX Monoclonal antibodies specific for Wlms' tumour protein antigen WT1
PT - useful for detecting, monitoring and diagnosing malignancies
PT characterised by expression of WT1 protein, e.g. leukaemia
XX Claim 1; Page 42-43; 54pp; English.
XX The human Wlms' tumour antigen WT1 (sequence given in R85065) was used
CC as the basis for the design of a synthetic WT1 sequence (see R85066)
CC used to raise monoclonal antibodies specific for the antigen.
XX Sequence 429 AA:

Query Match          100.0%; Score 123; DB 16; Length 429;
Best Local Similarity 100.0%; Pred. No. 4,2e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMFPNAPYLPSCLE 23
   |||||||||||||||||||
Db 117 psgassgqarmfnpaylpsele 139

RESULT 9
W47176
ID W47176 standard; Protein; 449 AA.
XX
XX W47176:
XX 01-JUN-1998 (first entry)
DT Wlms' tumour polypeptide (WT1).
DE Wlms' tumour polypeptide (WT1).
XX Wlms' tumour; WT1; cancer treatment; antibody production; WAGR;
XX Denys-drash syndrome; WT1.
XX Homo sapiens.
XX US5726288-A.
XX 10-MAR-1998.
XX 02-AUG-1993; 93US-0102942.
XX 02-AUG-1993; 93US-0102942.
XX 02-AUG-1993; 93US-0102942.
XX 13-NOV-1989; 89US-0435780.
XX 13-NOV-1990; 90US-0614161.
XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX

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PI Bruening W, Buckler AJ, Call KM, Darveau A, Glaser TM;
PI Haber DA, Housman DE, Ito CY, Pelletier J, Rose EA;
XX WPI; 1998-192828/17.
XX New Wlms' tumour polypeptide - useful for, e.g. cancer treatment
XX and antibody production
XX Disclosure; Columns 39-42; 42pp; English.
XX This is a Wlms' tumour (WT1) polypeptide. The Wlms' tumour gene
XX (WT1) is associated with 11p3 locus on the human chromosome. The
XX polypeptide or immunogenic fragments of the polypeptide can be used to
XX treat cancerous or precancerous conditions (especially Wlms' tumour), or
XX to raise antibodies for diagnostic use. The product allow detection of
XX risk of development of Wlms' tumour, e.g. in diseases such as WAGR and
XX Denys-Drash syndrome, to be assessed prior to current methods of
XX detection.
XX Sequence 449 AA:

Query Match          100.0%; Score 123; DB 19; Length 449;
Best Local Similarity 100.0%; Pred. No. 4.4e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMFPNAPYLPSCLE 23
   |||||||||||||||||||
Db 117 psgassgqarmfnpaylpsele 139

RESULT 10
Y98804
ID Y98804 standard; Protein; 449 AA.
XX
XX Y98804:
XX 31-JUL-2000 (first entry)
DT Human WT1 protein sequence SEQ ID NO:319.
DE Human WT1 protein sequence SEQ ID NO:319.
XX WT1; immunotherapy; immunogenic; malignant disease; cancer; leukaemia;
XX metastatic disease; mouse; human; Wlms' tumour; Immune response;
XX vaccine.
XX Homo sapiens.
XX WO200018795-A2.
XX 06-APR-2000.
XX 30-SEP-1999; 99WO-US22819.
XX 30-SEP-1998; 98US-0164223.
XX 25-MAR-1999; 99US-0276484.
XX (CORI-) CORIXA CORP.
XX (GAIG/) GAIGER A.
XX Gaiger A, Cheever M;
XX WPI; 2000-293107/25.
XX Novel polypeptides comprising an immunogenic portion of a native WT1
XX polypeptide, useful for inhibiting the development of malignant
XX diseases associated with WT1 expression e.g. leukemia or cancer
XX Disclosure; Page 190-191; 193pp; English.
XX The present invention describes polypeptides (I) comprising an
XX immunogenic portion of a native Wlms' tumour gene product polypeptide,
XX WT1, (or variants of the immunogenic portion retaining the ability to
XX react with WT1-specific antisera and/or T-cell lines or clones) and
XX

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CC comprising 16 consecutive amino acids (aa) or less of a native WT1
CC polypeptide. The polypeptides are useful therapeutically and to
CC manufacture medicaments for enhancing/inducing an immune response in
CC patients. The polypeptides, mimetics or polynucleotides can be included
CC with a carrier/excipient in pharmaceutical compositions or with a
CC non-specific immune response enhancer (e.g. an adjuvant or enhancer
CC preferentially enhancing a T cell response) in vaccines. Pharmaceutical
CC compositions and vaccines can be administered to human patients to
CC enhance or induce an immune response specific for WT1 or a cell
CC expressing WT1, useful to inhibit the development of malignant diseases
CC associated with WT1 expression, e.g. leukemia (especially acute/chronic
CC myeloid leukemia or acute lymphocytic leukemia) or cancer (especially
CC breast, lung, thyroid or gastrointestinal cancer, or a melanoma). Y98501
CC to Y98811 represent polypeptide sequences, and A13848 to A13862 represent
CC PCR primers, used in the exemplification of the present invention.

SQ Sequence 449 AA;

Query Match 100.0%; Score 123; DB 21; Length 449;
Best Local Similarity 100.0%; Pred. No. 4.4e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMPNAPYLPSCLE 23
Db 117 psqassgqarmfnapylpscle 139

RESULT 11

Y98805 ID Y98805 standard; protein; 449 AA.

AC Y98805;

DT 31-JUL-2000 (first entry)

DE Mouse WT1 protein sequence SEQ ID NO:320.

KW WT1; immunotherapy; immunogenic; malignant disease; cancer; leukemia;
KW metastatic disease; mouse; human; Wilm's tumour; immune response;
KW vaccine.

OS Mus musculus.

PN WO200018795-A2.

PD 06-APR-2000.

PF 30-SEP-1999; 99WO-US22819.

PR 30-SEP-1998; 98US-0164223.

PR 25-MAR-1999; 99US-0276484.

PA (COR1-) CORIXA CORP.

PA (GAIG/) GAIGER A.

PI Gaiger A, Cheever M;

DR WPI: 2000-293107/25.

PT Novel polypeptides comprising an immunogenic portion of a native WT1

PT polypeptide, useful for inhibiting the development of malignant

PT diseases associated with WT1 expression e.g. leukemia or cancer

PS Disclosure: Page 191-192; 193pp; English.

CC The present invention describes polypeptides (I) comprising an

CC immunogenic portion of a native Wilm's Tumour gene product polypeptide,
CC WT1, (or variants of the immunogenic portion retaining the ability to
CC react with WT1-specific antisera and/or T-cell lines or clones) and
CC comprising 16 consecutive amino acids (aa) or less of a native WT1
CC polypeptide. The polypeptides are useful therapeutically and to
CC manufacture medicaments for enhancing/inducing an immune response in

CC patients. The polypeptides, mimetics or polynucleotides can be included
CC with a carrier/excipient in pharmaceutical compositions or with a
CC non-specific immune response enhancer (e.g. an adjuvant or enhancer
CC preferentially enhancing a T cell response) in vaccines. Pharmaceutical
CC compositions and vaccines can be administered to human patients to
CC enhance or induce an immune response specific for WT1 or a cell
CC expressing WT1, useful to inhibit the development of malignant diseases
CC associated with WT1 expression, e.g. leukemia (especially acute/chronic
CC myeloid leukemia or acute lymphocytic leukemia) or cancer (especially
CC breast, lung, thyroid or gastrointestinal cancer, or a melanoma). Y98501
CC to Y98811 represent polypeptide sequences, and A13848 to A13862 represent
CC PCR primers, used in the exemplification of the present invention.

SQ Sequence 449 AA;

Query Match 100.0%; Score 123; DB 21; Length 449;
Best Local Similarity 100.0%; Pred. No. 4.4e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMPNAPYLPSCLE 23
Db 117 psqassgqarmfnapylpscle 139

RESULT 12

Y80196 ID Y80196 standard; protein; 449 AA.

AC Y80196;

DT 24-MAY-2000 (first entry)

DE Mouse Wilm's tumour suppressor gene WT1 product SEQ ID NO:1.

KW Wilm's tumour suppressor gene; WT1; cancer; antigen; vaccine; MHC;

KW major histocompatibility complex; leukemia; tumour; antitumour.

OS Mus sp.

PN WO200006602-A1.

PD 10-FEB-2000.

PF 30-JUL-1999; 99WO-JP04130.

PR 31-JUL-1998; 98JP-0218093.

PA (SUGI/) SUGIYAMA H.

PI Sugiyama H, Oka Y;

DR WPI: 2000-195264/17.

PT Cancer antigens based on Wilm's tumor suppressor gene WT1 product or

PT peptide derivatives, for cancer vaccines in treating leukemia and solid

PT tumors e.g. stomach cancer, skin cancer, lung cancer and breast cancer

PS Claim 2; Page 38-40; 48pp; Japanese.

CC The present invention describes a cancer antigen containing the active
CC component of Wilm's tumour suppressor gene WT1 product, or partial
CC peptides, for cancer vaccines in treating leukemia and solid tumours.
CC The cancer antigens are useful for cancer vaccines in treating
CC leukemia, bone-marrow abnormal formation syndrome, malignant lymphoma,
CC multiple myeloma, stomach cancer, cancer of the large intestine, lung
CC cancer, breast cancer, blastoma, liver cancer, skin cancer, bladder
CC cancer, prostate cancer, uterus cancer, cervical cancer, or ovary
CC cancer. The present sequence represents the mouse Wilm's tumour
CC suppressor gene WT1 product.

SQ Sequence 449 AA;

Query Match 100.0%; Score 123; DB 21; Length 449;
 Best Local Similarity 100.0%; Pred. No. 4,4e-12;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PSQASSGOARMPNAPYLPSCLE 23
 ||||||||||||||||||||
 DB 117 psqassgqarmfnapylpscle 139

RESULT 13

ID Y80197 standard; protein; 449 AA.

XX Y80197;

DT 24-MAY-2000 (first entry)

XX Human Wilms' tumour suppressor gene WT1 product SEQ ID NO:2.

XX Wilm's tumour suppressor gene; WT1; cancer; antigen; vaccine; MHC;

KW major histocompatibility complex; leukaemia; tumour; antitumour.

XX Homo sapiens.

XX WO200006602-A1.

XX 10-FEB-2000.

PF 30-JUL-1999; 99WO-JP04130.

XX 31-JUL-1998; 98JP-0218093.

XX (SUGI/) SUGIYAMA H.

XX Sugiyama H, Oka Y;

XX WPI; 2000-195264/17.

PT Cancer antigens based on Wilm's tumor suppressor gene WT1 product or

PT peptide derivatives, for cancer vaccines in treating leukemia and solid

XX tumors e.g. stomach cancer, skin cancer, lung cancer and breast cancer

XX Claim 2; Page 40-42; 48pp; Japanese.

XX The present invention describes a cancer antigen containing the active

XX component of Wilms' tumour suppressor gene WT1 product, or partial

XX peptides, for cancer vaccines in treating leukaemia and solid tumours.

XX The cancer antigens are useful for cancer vaccines in treating

XX leukaemia, bone-marrow abnormal formation syndrome, malignant lymphoma,

XX multiple myeloma, stomach cancer, cancer of the large intestine, lung

XX cancer, breast cancer, blastoma, liver cancer, skin cancer, bladder

XX cancer, prostate cancer, uterus cancer, cervical cancer, or ovary

XX suppressor gene WT1 product.

XX Sequence 449 AA;

XX

XX

XX Y98810 standard; Peptide: 9 AA.

XX Y98810;

XX 31-JUL-2000 (first entry)
 DT WTI related peptide SEQ ID NO:325.
 DE WTI; immunotherapy; immunogenic; malignant disease; cancer; leukaemia;
 KW metastatic disease; mouse; human; Wilm's tumour; immune response;
 KW vaccine.
 XX Homo sapiens.
 OS Mus musculus.
 XX WO200018795-A2.
 XX 06-APR-2000.
 XX 30-SEP-1999; 99WO-US22819.
 XX 30-SEP-1998; 98US-0164223.
 XX 25-MAR-1999; 99US-0276484.
 XX (CORI-) CORIXA CORP.
 XX (GAIG/) GAIGER A.
 XX Galger A, Cheever M;
 XX WPI; 2000-293107/25.
 XX Novel polypeptides comprising an immunogenic portion of a native WTI
 PT polypeptide, useful for inhibiting the development of malignant
 XX diseases associated with WTI expression e.g. leukemia or cancer -
 XX Disclosure; Page 193; 193pp; English.

XX The present invention describes polypeptides (I) comprising an
 CC immunogenic portion of a native Wilm's Tumour gene product polypeptide,
 CC WTI, (or variants of the immunogenic portion retaining the ability to
 CC react with WTI-specific antisera and/or T-cell lines or clones) and
 CC comprising 16 consecutive amino acids (aa) or less of a native WTI
 CC polypeptide. The polypeptides are useful therapeutically and to
 CC manufacture medicaments for enhancing/inducing an immune response in
 CC patients. The polypeptides, mimetics or polynucleotides can be included
 CC with a carrier/exipient in pharmaceutical compositions or with a
 CC non-specific immune response enhancer (e.g. an adjuvant or enhancer
 CC preferentially enhancing a T cell response) in vaccines. Pharmaceutical
 CC compositions and vaccines can be administered to human patients to
 CC enhance or induce an immune response specific for WTI or a cell
 CC expressing WTI, useful to inhibit the development of malignant diseases
 CC associated with WTI expression, e.g. leukemia (especially acute/chronic
 CC myeloid leukemia or acute lymphocytic leukemia) or cancer (especially
 CC breast, lung, thyroid or gastrointestinal cancer, or a melanoma). Y98501
 CC to Y98811 represent polypeptide sequences, and A13848 to A13862 represent
 CC PCR primers, used in the exemplification of the present invention.

XX Sequence 9 AA;

XX

Query Match 44.7%; Score 55; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e-05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 PNAPYLPSC 21
 |||||||||

DB 1 pnaylpssc 9

RESULT 15

ID Y98809 standard; Peptide: 9 AA.

XX Y98809;

XX 31-JUL-2000 (first entry)

XX WT1 related peptide SEQ ID NO:324.
DE
XX

KW WT1: Immunotherapy; immunogenic; malignant disease; cancer; leukemia;
metastatic disease; mouse; human; Wilm's tumour; Immune response;
KW vaccine.

XX Homo sapiens.
OS Mus musculus.

XX WO200018795-A2.

XX PD 06-APR-2000.

XX PF 30-SEP-1999; 99WO-US22819.

XX PR 30-SEP-1998; 98US-0164223.
PR 25-MAR-1999; 99US-0276484.

XX (CORI-) CORIXA CORP.
PA (GAIG/) GAIGER A.

XX PI Galger A, Cheever M;

XX DR WPI: 2000-293107/25.

XX Novel polypeptides comprising an immunogenic portion of a native WT1
PT polypeptide, useful for inhibiting the development of malignant
PT diseases associated with WT1 expression e.g. leukemia or cancer
PS
PS Disclosure: Page 193; 193pp; English.

CC The present invention describes polypeptides (I) comprising an
CC immunogenic portion of a native Wilm's Tumour gene product polypeptide,
CC WT1. (Or variants of the immunogenic portion retaining the ability to
CC react with WT1-specific antisera and/or T-cell lines or clones) and
CC comprising 16 consecutive amino acids (aa) or less of a native WT1
CC polypeptide. The polypeptides are useful therapeutically and to
CC manufacture medicaments for enhancing/inducing an immune response in
CC patients. The polypeptides, mimetics or polynucleotides can be included
CC with a carrier/exipient in pharmaceutical compositions or with a
CC non-specific immune response enhancer (e.g. an adjuvant or enhancer
CC preferentially enhancing a T cell response) in vaccines. Pharmaceutical
CC compositions and vaccines can be administered to human patients to
CC enhance or induce an immune response specific for WT1 or a cell
CC expressing WT1, useful to inhibit the development of malignant diseases
CC associated with WT1 expression, e.g. leukemia (especially acute/chronic
CC myeloid leukemia or acute lymphocytic leukemia) or cancer (especially
CC breast, lung, thyroid or gastrointestinal cancer, or a melanoma). Y98501
CC to Y98811 represent polypeptide sequences, and A13848 to A13862 represent
CC PCR primers, used in the exemplification of the present invention.
XX

XX Sequence 9 AA;

Query Match

43.1%; Score 53; DB 21; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.1e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MFPNAPYLP 19

Db 1 mfpnapyip 9

Search completed: April 11, 2001, 14:01:57
Job time: 519 sec